

GenCore version 5.1.4 p5 4578
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CM nucleic - nucleic search, using sw model

Run on: May 16, 2003, 17:37:19 ; Search time 177 Seconds
(without alignments)
10560.218 Million cell updates/sec

File: US-09-358-321c-31

Perfect score: 830

Sequence: 1 tctagaatggttaagcgctat.....ctgaattagtagcgccgcg 830

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_101002:*

- 1: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
- 2: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
- 5: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
- 6: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
- 7: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:*
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- 9: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
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- 11: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:*
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- 13: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
- 14: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:*
- 15: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:*
- 16: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:*
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- 18: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:*
- 19: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:*
- 20: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*
- 21: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	830	100.0	830	21	AAA92442
2	528	63.6	828	21	AAA92439
3	528	63.6	828	22	AAH78144
4	528	63.6	828	24	ABK71323
5	528	63.6	828	24	ABA04520
6	526.4	63.4	828	21	AAA92443
7	526.4	63.4	828	22	AAH78148
8	526.4	63.4	828	24	ABK71327
9	526.4	63.4	828	24	ABA04524

10	521.4	62.8	819	21	AAA92442	Plasmid pCHOM1 MAB
11	521.4	62.8	819	22	AAH78147	Nucleotide sequenc
12	521.4	62.8	819	24	ABK71326	DNA encoding throm
13	521.4	62.8	819	24	ABA04523	Murine MABL-1 #4 c
14	519.8	62.6	819	21	AAA92444	Plasmid pCHOM2 MAB
15	519.8	62.6	819	22	AAH78149	Nucleotide sequenc
16	519.8	62.6	819	24	ABK71328	DNA encoding throm
17	519.8	62.6	819	24	ABA04525	Murine MABL-2 #4 c
18	518.4	62.5	1605	22	AAH78156	Nucleotide sequenc
19	518.4	62.5	1605	24	ABK71335	DNA encoding throm
20	518.4	62.5	1605	24	ABA04532	Murine MABL-2 #6 c
21	512.4	61.7	741	22	AAH78153	Nucleotide sequenc
22	512.4	61.7	741	24	ABK71332	DNA encoding throm
23	512.4	61.7	741	24	ABA04529	Murine MABL-2 #5 c
24	510.8	61.5	876	19	AAV10390	Monoclonal antibod
25	501.2	60.4	1637	21	AAZ88358	Bispecific anti-ze
26	499	60.1	753	20	AAH77245	Mouse scFv fragmen
27	499	60.1	753	20	AAH77241	Mouse scFv fragmen
28	486	58.6	780	22	AAH78172	Nucleotide sequenc
29	486	58.6	780	24	ABK71351	DNA encoding throm
30	486	58.6	780	24	ABA04548	Murine MABL-2 #7 c
31	476	57.3	753	22	AAF60025	DNA encoding singl
32	476	57.3	792	22	AAF60021	DNA encoding S19 S
33	447	53.9	459	21	AAZ61045	Nucleotide sequenc
34	444	53.5	792	22	AAF60022	DNA encoding singl
35	443.4	53.4	786	22	AAF60026	DNA encoding singl
36	423.4	51.0	438	21	AAZ61046	Nucleotide sequenc
37	419.4	50.5	1135	20	AAH58936	Plasmid pJG718 enc
38	415	50.0	1047	20	AAZ21156	Artificial synthe
39	415	50.0	1086	20	AAZ21158	Artificial synthe
40	411.6	49.6	768	17	AAH48000	Coding sequence fo
41	409.4	49.3	729	19	AAH36236	DNA of ScFv 421 wh
42	408.2	49.2	753	21	AAZ61064	Heavy chain of an
43	407.6	49.1	749	18	AAH86234	Anti-human protein
44	405.2	48.8	1611	18	AAH86221	Human p53 protein
45	401.4	48.4	726	20	AAH86942	Antibody B10C7 enc

ALIGNMENTS

RESULT 1
AAZ61047
ID AAZ61047 standard; DNA; 830 BP.
AC AAZ61047;
XX
DT 30-MAY-2000 (first entry)
DE DNA encoding a single chain anti-delta9-desaturase antibody.
KW Delta9-desaturase; antibody; transit peptide; passenger protein;
KW plant cell organelle; maize; stearoyl-ACP-delta9-desaturase;
KW transgenic plant; ss.
XX
OS Synthetic.
OS Mus sp..
XX
FH Key Location/Qualifiers
CDS 7..813
FT /tag= a
FT /note= "no termination codon given"
FT mat_peptide 67..813
FT /tag= b
XX
XX WO200005391-A1.
PN
XX
XX
PD 03-FEB-2000.
XX
XX
PF 21-JUL-1999; 99WO-US16405.
XX
XX 21-JUL-1998; 98US-0093587.
PR
XX

511 TCTTGAGATCTAGTCAGAGCCCTTTACACAGTAATGAATCACCTATTATACATTGGTAC 570
 526 TCTTGAGATCTAGTCAGAGCCCTTTACACAGTAATGAATCACCTATTATACATTGGTAC 585
 571 CTGACAGAGCCAGGCGAGTCTCAAGAGCTCTGATCTACAAAGTTTCCAAACCGATTTCCT 630
 586 CTACAGAGAGCCAGGCGAGTCTCAAGAGCTCTGATCTACAAAGTTTCCAAACCGATTTCCT 645
 631 GGGGTCCACAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTACACTCAGATCAGC 690
 646 GGGGTCCACAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTACACTCAGATCAGC 705
 691 AGAGTGGAGGCTGAGGATCTGGAGGTTTATTTCTGCTCTCAAAAGTACACATGTTCCGGTAC 750
 706 AGAGTGGAGGCTGAGGATCTGGAGGTTTATTTCTGCTCTCAAAAGTACACATGTTCCGGTAC 765
 751 ACCTTGGAGGGGGGACCAAGCTGGAAATAAAGAGAAAAA 792
 766 ACCTTGGAGGGGGGACCAAGCTGGAAATAAAGAGACTACAAA 807

RESULT 4

ABK71323
 ID ABK71323 standard; DNA; 828 BP.

ABK71323;

30-JUL-2002 (first entry)

DNA encoding thrombopoietin agonist antibody associated protein #5.

Modified antibody; thrombopoietin; TPO; agonist;
 TPO receptor; platelet reduction-associated blood disease;
 thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction;
 gene; ds.

Mus sp.

WO200233072-A1.

25-APR-2002.

22-OCT-2001; 2001WO-JP09259.

20-OCT-2000; 2000JP-0321821.

17-APR-2001; 2001WO-JP03288.

12-SEP-2001; 2001JP-0277314.

(CHUS) CHUGAI SEIYAKU KK.

Tsuchiya M, Ohtomo T, Yabuta N, Tsunoda H, Orita T;

WPI: 2002-383513/41.

P-PSDB; ABG35311.

Degraded thrombopoietin agonist antibodies containing H and L chain V domains of monoclonal antibody, useful in preventives and/or remedies for blood diseases, thrombocytopenia following cancer chemotherapy or leukaemia

Example 5; Page 147-148; 213pp; Japanese.

The invention describes a modified antibody comprising at least 2 heavy chain variable domains and 2 or more light chain variable domains of an antibody, and exhibits thrombopoietin (TPO) agonistic effect by causing the TPO receptor to crosslink. The antibodies are useful in preventives and/or remedies for platelet reduction-associated blood diseases, thrombocytopenia following cancer chemotherapy or leukaemia. The antibody can act as a TPO signal transduction agonist by transducing a signal into cells by crosslinking a TPO receptor to exert TPO agonism. This sequence encodes a thrombopoietin (TPO) agonist antibody associated protein.

SQ Sequence 828 BP; 211 A; 201 C; 223 G; 193 T; 0 other;
 Query Match 63.6%; Score 528; DB 24; Length 828;
 Best Local Similarity 82.9%; Pred. No. 1.5e-139;
 Matches 632; Conservative 0; Mismatches 115; Indels 15; Gaps 2;
 QY 46 GCGGCGCATTCCTGCTTGGCGCGGTTCAACTGCAGCAGTCTGGGGCTGAGCTGGTGAGG 105
 DB 46 GCTGCCAACACAGCCATGGCGAGGTCCAGCTGCAGCAGTCTGGACCTGACCTGGTAAAG 105
 QY 106 CTTGGGGCTTCACTGACGCTGCTCTGCAAGGCTTCGGGCTACACATTTTACTGACTATGAA 165
 DB 106 CTTGGGGCTTCACTGACGATGCTCTGCAAGGCTTCGGGCTACACATTTTACTGACTATG 165
 QY 166 ATACACTGGGTGAGCAGACACCTGTGATGCGCTGGATGGATGGAGCTATTGATCTCT 225
 DB 166 ATGCACTGGGTGAAGCAAGCCAGGCGAGGCTTGGATGGATGATATATTTATCTCT 225
 QY 226 GAAACTGGTGGTACTGCTTACAACTCAGAAAGTTTCAAGGCAAGGCCATAGTGACTGTAGAC 285
 DB 226 TACAATGATGGTACTAAGTACAAATGAGAAAGTTTCAAGGCAAGGCCACACTGACTTCAGAG 285
 QY 286 AAATCCTCAGCAGCCTTACATGGAGCTCCGACCTCCGACATCTGAAGACTCTCCGGTC 345
 DB 286 AAATCCTCAGCAGCCTTACATGGAGCTCAGCAGCTGGGCTCTGAGGACTCTCGGGTC 345
 QY 346 TATTACTATACAGATGG-----TTTGGAGCTGGGGCAAGGGACTCTGGTC 393
 DB 346 TACTACTGTGAAGAGGGGGTTACTATAGTTACGACGACTGGGGCAAGGCCACTCTC 405
 QY 394 ACTGTCTCTGCA---GAGGTAAATCCTCAGGATCTGGCTCGGAATCCAAACCCGGGAT 450
 DB 406 ACAGTCTCTCAGTGGTGGTGGTTCGGGTGGTGGTGGTTCGGGTGGTGGGATCGGAT 465
 QY 451 GTTGTGATGACCCCAACCCACTCTCCCTGCTGCTGCTGCTTGGAGATCAAGCCTCCATC 510
 DB 466 GTTGTGATGACCCCAACCTCTCCCTGCTGCTGCTGCTTGGAGATCAAGCCTCCATC 525
 QY 511 TCTTCAGATCTAGTCAGAGCCTTTTACACAGTATGAATCAACCTATTATACATTGGTAC 570
 DB 526 TCTTCAGATCTAGTCAGAGCCTTTTACACAGTAAAGAAACACCTATTATCAATGGTAC 585
 QY 571 CTGAGAAAGCCAGGCGAGTCTCCAAAGCTCTCTGATCTACAAAGTTTCCAAACCGATTTCCT 630
 DB 586 CTACAGAGAGCCAGGCGAGTCTCCAAAGCTCTCTGATCTACAAAGTTTCCAAACCGATTTCCT 645
 QY 631 GGGTCCACAGACAGGTTTCAGTGGCAGTGGATCAGGAGCAGATTTTCACTCAAGATCAGC 690
 DB 646 GGGTCCACAGACAGGTTTCAGTGGCAGTGGATCAGGAGCAGATTTTCACTCAAGATCAGC 705
 QY 691 AGAGTGGAGGCTGAGGATCTGGAGTGTATTTCTGCTCTCAAGATACACATGTTCCGGTAC 750
 DB 706 AGAGTGGAGGCTGAGGATCTGGAGTGTATTTCTGCTCTCAAGATACACATGTTCCGGTAC 765
 QY 751 ACGTTCCGAGGGGGGACCAAGCTGGAAATAAAGAGAAAAA 792
 DB 766 ACGTTCCGAGGGGGGACCAAGCTGGAAATAAAGAGACTACAAA 807

RESULT 5

ABA04520

ID ABA04520 standard; DNA; 828 BP.

XX ABA04520;

XX ABA04520;

XX 15-FEB-2002 (first entry)

XX Murine MABL-1 #3 coding sequence.

XX Murine; cytostatic; antiinflammatory; antianaemic; vasotropic;
 XX antibody; signal transduction; cancer; inflammation; hormonal disorder;
 XX leukaemia; lymphoma; aplastic anaemia; skeletal malformation; ds.

CC pscM2 MABL2-scFv, which is used in an example from the present
XX invention.
SQ Sequence 828 BP; 210 A; 199 C; 219 G; 200 T; 0 other;
Query Match 63.4%; Score 526.4; DB 21; Length 828;
Best Local Similarity 82.8%; Pred. No. 4.4e-139;
Matches 631; Conservative 0; Mismatches 116; Indels 15; Gaps 2;
2y 46 GCGCGCATTCCTCGCTTGGCGGCTTCAACTGCACAGTCTGGGCTGAGCTGGTGGAG 105
yb 46 GCTGCCCAACAGCCATGGCGAGTCCAGCTGCACAGTCTGGACCTGAACCTGGAAG 105
2y 106 CTGGGGCTTCAGTGACGCTGTCTCTCAAGGCTTCGGGTACACATTTACTGACTATGAA 165
yb 106 CTGGGGCTTCAGTGAAGTGTCTCTCAAGGCTTCGGGTACACATTTACTGACTATGAA 165
2y 166 ATACACTGGGTGAGGAGACACCTGTGCATGGCTCGAATGGATTGGAGCTATTGATCT 225
yb 166 ATTCACCTGGGTGAAGCAGAGAGCCAGGCGAGGCTTGGTGGATTGGATATATTATCT 225
2y 226 GAAACTGGTGGTACTGCCTACAATCAGAAGTTCACGACAAAGGCCATAGTACTGTAGAC 285
yb 226 TACAATGATGGTACTAAGTATATAGAGTTCACGACAAAGGCCATCTGACTTCAGAC 285
2y 286 AAATCTCCAGCAGCCTACATGGAGCTCCGAGCTCGACATCTGAAGACTCTGCCGTC 345
yb 286 AAATCTCCAGCAGCCTACATGGAGCTCCGAGCTCGACATCTGAAGACTCTGCCGTC 345
2y 346 TATTACTATACAGATGG-----TTGAGGACTGGGGCAAGGACTCTGGTC 393
yb 346 TATTACTGTCAAGAGGGGTTACTATCTTACGACACTGGGGCAAGGCAACCACTCTC 405
2y 394 ACTGTCTCTGCA--GAGGTAAATCCTCAGGATCTGGCTCCGAATCCAAACCCGGGAT 450
yb 406 ACAGTCTCTCAGGTGGTGGTTCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 465
2y 451 GTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 510
yb 466 GTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 525
2y 511 TCTGAGATCTAGTCAGAGCCCTTTACACAGTAAATGGAATCACCTATTATGATGATG 570
yb 526 TCTGAGATCAAGTCAGAGCCCTTGGCAGAGTAAATGGAATCACCTATTATGATGATG 585
2y 571 CTGAGAAGCCAGGCGAGCTCTCAAGCTCTCTGATCTCAAAAGTTTCCAAACCGATTTC 630
yb 586 CTGAGAAGCCAGGCGAGCTCTCAAACTCTGATCTCAAAAGTTTCCAAACCGATTTC 645
2y 631 GGGTCCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTACACTCAAGATCAGC 690
yb 646 GGGTCCAGACAGGTTTCAGTGGCAGTGGATCAGTGGATCAGTGGATCAGTGGATCAG 705
2y 691 AGAGTGGAGGCTGAGGATCTGGAGTTTATTCTGCTCTCAAGTACACATGTTCCGTAC 750
yb 706 AGAGTGGAGGCTGAGGATCTGGAGTTTATTCTGCTCTCAAGTACACATGTTCCGTAC 765
2y 751 ACCTTCGGAGGGGGACCAAGCTGGAAATATAAAGAGAAATA 792
yb 766 ACCTTCGGAGGGGGACCAAGCTGGAAATATAAAGACTACAAA 807

RESULT 7

JAH78148
D AAH78148 standard; DNA; 828 BP.
X
X AAH78148;
X
X 26-NOV-2001 (first entry)
X
X Nucleotide sequence of a murine antibody L chain.
X
X Apoptosis; nucleated blood cell; integrin-associated protein; IAP;

KW erythrocyte agglutination; blood disease; leukemia; myeloma;
KW Hodgkin's disease; non-Hodgkin's lymphoma; ss.
XX Mus sp.
XX
XX Key Location/Qualifiers
FH CDS 1..825
FT /tag= a
FT /product= "L chain"
XX
XX WO200166737-A1.
XX
XX 13-SEP-2001.
XX
XX 12-MAR-2001; 2001WO-JP01912.
XX
XX 10-MAR-2000; 2000US-0523095.
XX 17-APR-2000; 2000JP-0115246.
XX 20-OCT-2000; 2000JP-0321822.
XX (CHUS) CHUGAI SEIVAKU KK.
XX
XX Fukushima N, Tsuchiya M, Oh-eda M, Uno S, Kikuchi Y;
XX
XX WPI; 2001-570772/64.
XX P-PSDB; AAG67495.
XX
XX Reconstituted polypeptide induces apoptosis in nucleated blood cells
XX that contain integrin-associated protein (IAP), is useful for the
XX treatment of blood diseases such as leukemia -
XX
XX Example 5; Page 113-115; 141pp; Japanese.
XX
XX The specification describes a reconstituted polypeptide, which
XX induces apoptosis in nucleated blood cells that contain
XX integrin-associated protein (IAP). The polypeptide binds to IAP
XX without causing agglutination of erythrocytes. The polypeptide
XX contains at least two H chain V domains and at least two L chain
XX V domains of a monoclonal antibody which induces apoptosis in
XX nuclear blood cells having IAP. The reconstituted polypeptide is used
XX for the treatment of blood diseases such as acute or chronic myeloid
XX leukemia, acute or chronic lymphoid leukemia, adult T-cell leukemia,
XX multiple myeloma, mixed leukemia, hairy cell leukemia, Hodgkin's
XX disease or non-Hodgkin's lymphoma. The present sequence encodes a
XX murine monoclonal antibody L chain, which is used in the course of
XX the invention.
XX
XX Sequence 828 BP; 210 A; 199 C; 219 G; 200 T; 0 other;
SQ

Query Match 63.4%; Score 526.4; DB 22; Length 828;
Best Local Similarity 82.8%; Pred. No. 4.4e-139;
Matches 631; Conservative 0; Mismatches 116; Indels 15; Gaps 2;
Qy 46 GCGCGCATTCCTCGCTTGGCGGCTTCAACTGCACAGTCTGGGCTGAGCTGGTGGAG 105
Db
Qy 46 GCTGCCCAACAGCCATGGCGAGTCCAGCTGCACAGTCTGGACCTGGAACCTGTAAG 105
Db
Qy 106 CTGGGGCTTCAGTGACGCTGTCTCTCAAGGCTTCGGGCTACACATTTACTGACTATGAA 165
Db 106 CTGGGGCTTCAGTGAAAGATGTCTCTCAAGGCTTCTGATACACCTTCGCTAACCATGTT 165
Qy 166 ATACACTGGGTGAGGAGACACCTGTGTCATGGCCCTGGAATGGATTGGAGCTATTGATCCT 225
Db 166 ATTCACCTGGGTGAGGAGAGAGCCAGGCGCTTCAGTGGATTGGATATATTATCT 225
Qy 226 GAAACTGGTGGTACTGCTTACATGAGAGTTTCAAGCAGAGGCCATGACTGTAGAC 285
Db 226 TACAATGATGGTACTAAGTATAATCAGAAGTTTCAAGCAGAGGCCACTCTGACTTCAGAC 285
Qy 286 AAATCTCCAGCAGCCTACATGGAGCTCCGAGCTCGACATCTGAGAGCTCTGCCGTC 345
Db 286 AAATCTCCAGCAGCCTACATGGAGCTCCGAGCTCGACATCTGAGAGCTCTGCCGTC 345


```

ID ABA04524 standard; DNA; 828 BP.
XX AC ABA04524;
XX DT 15-FEB-2002 (first entry)
XX DE Murine MABL-2 #3 coding sequence.
XX KW Murine; cytostatic; antiinflammatory; antianaemic; vasotropic;
XX KW antibody; signal transmission; cancer; inflammation; hormonal disorder;
XX KW leukaemia; lymphoma; aplastic anaemia; skeletal malformation; ds.
XX OS Mus sp.
XX Key Location/Qualifiers
CDS 1..825
   /tag= a
   /product= "Murine MABL-2 #3"
WO200179494-A1.
PD 25-OCT-2001.
XX 17-APR-2001; 2001WO-JP03288.
XX 17-APR-2000; 2000JP-0115246.
XX 20-OCT-2000; 2000JP-0321821.
XX 20-OCT-2000; 2000JP-0321822.
XX 12-MAR-2001; 2001WO-JP01912.
XX (CHUS ) CHUGAI SEIYAKU KK.
XX Fukushima N, Tsuchiya M, Oheda M, Uno S, Kikuchi Y, Ohtomo T;
XX WPI; 2002-066368/09.
XX P-PSDB; AAM47633.
XX Antibodies for treatment of diseases associated with cell
XX proliferation, hormonal disorders and cytokines comprise agonist
XX activity to signal transmission across cell membranes -
XX Example 5; Page 131-133; 173pp; Japanese.
XX IPS The present invention relates to modified antibodies. The antibodies
XX contain two or more H chain V domains and two or more L chain V domains
XX of a monoclonal antibody (Mab) which is capable of transmitting a signal
XX across the cell membrane by cross-linking a cell surface molecule, where
XX the antibodies can serve as signal transmission agonists. The antibodies
XX are useful for treatment and prevention of a broad range of disorders in
XX which signal transmission is implicated, such as cancer, inflammation,
XX hormonal disorders, leukaemia, malignant lymphoma, aplastic anaemia, and
XX skeletal malformations. The present sequence was used to illustrate the
XX present invention.
XX SQ Sequence 828 BP; 210 A; 199 C; 219 G; 200 T; 0 other;
Query Match 63.4%; Score 526.4; DB 24; Length 828;
Best Local Similarity 82.8%; Pred. No. 4.4e-139;
Matches 631; Conservative 0; Mismatches 116; Indels 15; Gaps 2;
2y 46 GGGGCGCATTCCTCCCTTGGCGGGTTTCAACTCAGCAGTCTGGGCTCAGCTGTGGAGG 105
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
46 GCTGCCCAACCAAGCCATGGCGCAGGTCCAGCTCAGCAGTCTGGACCTGAACCTGGTAAG 105
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2y 106 CTTGGGGCTTCAGTGACGCTGTCTCTCAAGGCTTCGGGCTACACATTTACTGACTATGAA 165
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
106 CTTGGGGCTTCAGTGAAAGATGTCTCTCAAGGCTTCCTGGATACACCTTCGTAACCATGTT 165
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2y 166 ATACACTGGGTGAGGAGCAGACCTGTGCATGGCTGGAATGGATTCGAGCTATTGATCCT 225
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   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2y 166 ATTCACTGGGTGAAGCAGAGCAGGCGGCGGCTTCAGTGGATTGGATATATTATCTCT 225
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2y 226 GAAACTGGTGTACTGCTTACAATCAGAAAGTTCAAGAGCAAGGCCATAGTACTGTAGAC 285
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Qy 346 TATTACTATACAAGATGG-----TTTGAGGACTGGGGCCAAAGGGACTCTGGTC 393
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Db 346 TATTACTGTGCAAGAGGGGTTACTATATTACGACGACTGGGGCCAAAGGCCACTCTC 405
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Qy 394 ACTGTCTCTGCA---GAGGGTAAATCTCAGGATCTGGCTCCGAATCCAAACCCGGGGAT 450
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 451 GTTGTGATGACCCCAACCCACTCTCCCTGCTGTCTGCTCTTGGAGATCAAGCCTCCATC 510
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 466 GTTGTGATGACCCCAAGTCCACTCTCCCTGCTGTCTGCTCTTGGAGATCAAGCCTCCATC 525
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 511 TCTTCAGATCTAGTCAGAGCCTTTTACACAGTAATGAATCACCTATTTACATTGGTAC 570
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 526 TCTTCAGATCAAGTCAGAGCCTTGTGCACAGTAATGAAGAACCTATTTACATTGGTAC 585
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 571 CTGCAGAACCCAGGCCAGTCTCCAAAGCTCTCTGATCTACAAAGTTTCCAAACCGATTTCT 630
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 586 CTGCAGAACCCAGGCCAGTCTCCAAAGCTCTCTGATCTACAAAGTTTCCAAACCGATTTCT 645
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 631 GGGGTCCAGACAGGTTTCAGTGGCAGTGGATCAGGAGCAGATTTACACTCAAGATCAGC 690
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 646 GGGGTCCAGACAGGTTTCAGTGGCAGTGGATCAGTGCAGAGATTTACACTCATGATCAGC 705
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 691 AGAGTGGAGGCTGAGGATCTGGGAGTTTATTCTCTCTCAAAGTACACATGTTCCGCTAC 750
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 706 AGAGTGGAGGCTGAGGATCTGGGAGTTTATTCTCTCTCAAAGTACACATGTTCCGCTAC 765
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 751 ACGTTCCGAGGGGGACCAAGCTGGAATATAAAGAGAAAAA 792
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 766 ACGTTCCGAGGGGGACCAAGCTGGAATATAAAGACTACAAA 807
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
RESULT 10
AAA92442
ID AAA92442 standard; DNA; 819 BP.
XX AC AAA92442;
XX DT 15-JAN-2001 (first entry)
XX DE Plasmid pCHOM1 MABLI-scFv nucleotide sequence SEQ ID NO:23.
XX KW Monoclonal antibody; MABL; IAP; integrin associated protein;
XX KW single stranded Fv; apoptosis; blood disease; leukaemia;
XX KW cytostatic; ds.
XX OS Mus sp.
XX WO2000053634-A1.
XX PD 14-SEP-2000.
XX PF 10-MAR-2000; 2000WO-JP01458.
XX PR 10-MAR-1999; 99JP-0063557.
XX PA (CHUS ) CHUGAI SEIYAKU KK.
XX PI Fukushima N, Uno S;
XX WPI; 2000-587428/55.
XX P-PSDB; AAB23818.
XX Single stranded Fv antibody fragment inducing apoptosis in nucleated
XX blood cells having integrin associated protein for treatment of
```


Leukemia

Example 5; Page 62-64; 73pp; Japanese.

The present invention describes a polypeptide containing the variable region of the light chain of a monoclonal antibody, which induces apoptosis in nucleated blood cells having integrin associated protein (IAP). Also described are: (1) DNA encoding the novel polypeptide; (2) animal or microbial cells expressing the DNA of (1); and (3) agents for the treatment of blood disorders which contain the polypeptide. The polypeptide can be used in the treatment of blood disorders such as leukemia. The present sequence encodes the protein sequence from pCHOM1 NABU1-scrv, which is used in an example from the present invention.

Sequence 819 BP; 208 A; 195 C; 223 G; 193 T; 0 other;

Query Match 62.8%; Score 521.4; DB 21; Length 819;

Best Local Similarity 81.8%; Pred. No. 1.1e-137; Mismatches 126; Indels 15; Gaps 2;

Matches 632; Conservative 0;

35 TTTTGGCGGGCGGGCGGCAATTCCTGCTTTTGGCGGGTTCAACTGCAGCAGCTCTGGGGCTG 94
36 TCTTGGTAGCAACAGCTACAGGTGTCGACTCCAGGTCCAGCTGCAGCAGCTCTGGACCTG 85
37 AGCTGTGAGGCGCTGGGGCTTCAGTGACGCTGCTCTGCAAGGCTTCGGGTACACATTTA 154
38 ACCTGGTAAAGCCTGGGGCTTCAGTGAAGATGCTCTGCAAGGCTTCGGATACACACCTTCG 145
39 CTGACTATGAATATACACTGGGTGAGGAGACACCTGTGCATGGCTGGATGGATGGAG 214
40 TTAACCATGTTATGCACTGGGTGAAGCAGAGGCGAGGCGAGGCGCTTGAAGTGGAT 205
41 CTATTGATCTGAACTGGTGTACTCCCTACAAATCAGAAAGTTCAAGGCAAGGCCATAG 274
42 ATATTATCTTACATGATGTTACTAAGTACATGAGAAAGTTCAAGGCGAGGCCACAC 285
43 TGACTGTAGCAAAATCTCCAGCAGACAGCTACATGGAGCTCCGAGCTCCGATCTGAAG 334
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45 ACTCTGCCGTCTATTACTATACAGATGG-----TTTGAGGACTGGGGCAAG 382
46 ACTCTGCCGTCTACTACTGTGCAAGAGGGGGTTACTATAGTTACGAGACTGGGGCAAG 385
47 GGACTCTGGTCACTGTCTCTGCA---CAGGTTAAATCCTCAGGATCTGGCTCCGAATCCA 439
48 GCACCACTCTCAGACTCTCTCAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 445
49 AACCCGGGGATGTTGTGATGACCCCAACCACTCTCCCTGCTGTCAGTCTTTGGAGATC 499
50 CGGATCGGATGTTGTGATGACCCCAACCACTCTCCCTGCTGTCAGTCTTTGGAGATC 505
51 AAGCTCCATCTCTTGAGATCTAGTCAGAGCCCTTTACACAGTAAATGGAATCACCTATT 559
52 AAGCTCCATCTCTTGAGATCTAGTCAGAGCCCTTTACACAGTAAATGGAATCACCTATT 565
53 TACATGTTGATCTGCAAGCAGGCGAGCTCTCAAAAGCTCTGATCTACAAAGTTTCCA 619
54 TACATGTTGATCTGCAAGCAGGCGAGCTCTCAAAAGCTCTGATCTACAAAGTTTCCA 625
55 ACCGATTTCTGGGGTCCAGACAGAGTTTCAGTGGCAGTGGATCAGGAGACATTTACAC 679
56 ACCGATTTCTGGGGTCCAGACAGAGTTTCAGTGGCAGTGGATCAGGAGACATTTACAC 685
57 TCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGAGTTTATTTCTGCTCTCAAAAGTAC 739
58 TCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGAGTTTATTTCTGCTCTCAAAAGTAC 745
59 ATGTTCCGTACAGCTTCGAGGGGGGACCAAGCTGGAAATAAAGAGRAAAA 792
60 ATGTTCCGTACAGCTTCGAGGGGGGACCAAGCTGGAAATAAAGAGTACAAA 798

RESULT 11

AAH78147

ID AAH78147 standard; DNA; 819 BP.

XX AC AAH78147;

XX DT 26-NOV-2001 (first entry)

XX DE Nucleotide sequence of a murine antibody L chain.

XX KW Apoptosis; nucleated blood cell; integrin-associated protein; IAP;

XX KW erythrocyte agglutination; blood disease; leukemia; myeloma;

XX KW Hodgkin's disease; non-Hodgkin's lymphoma; ss.

XX OS Mus sp.

XX FH Key Location/Qualifiers

XX FT CDS 1..816

XX FT /tag= a

XX FT /product= "L chain"

XX PN WO200166737-A1.

XX PD 13-SEP-2001.

XX PF 12-MAR-2001; 2001WO-JP01912.

XX PR 10-MAR-2000; 2000US-0523095.

XX PR 17-APR-2000; 2000JP-0115246.

XX PR 20-OCT-2000; 2000JP-0321822.

XX PA (CHUS) CHUGAI SEIYAKU KK.

XX PI Fukushima N, Tsuchiya M, Oh-eda M, Uno S, Kikuchi Y;

XX DR WPI: 2001-570772/64.

XX DR P-PSDB; AAG67494.

XX PT Reconstituted polypeptide induces apoptosis in nucleated blood cells

XX PT that contain integrin-associated protein (IAP), is useful for the

XX PT treatment of blood diseases such as leukemia

XX PT Example 5; Page 111-113; 141pp; Japanese.

XX CC The specification describes a reconstituted polypeptide, which

XX CC induces apoptosis in nucleated blood cells that contain

XX CC integrin-associated protein (IAP). The polypeptide binds to IAP

XX CC without causing agglutination of erythrocytes. The polypeptide

XX CC contains at least two H chain V domains and at least two L chain

XX CC V domains of a monoclonal antibody which induces apoptosis in

XX CC nuclear blood cells having IAP. The reconstituted polypeptide is used

XX CC for the treatment of blood diseases such as acute or chronic myeloid

XX CC leukemia, acute or chronic lymphoid leukemia, adult T-cell leukemia,

XX CC multiple myeloma, mixed leukemia, hairy cell leukemia, Hodgkin's

XX CC disease or non-Hodgkin's lymphoma. The present sequence encodes a

XX CC murine monoclonal antibody L chain, which is used in the course of

XX CC the invention.

XX SQ Sequence 819 BP; 208 A; 195 C; 223 G; 193 T; 0 other;

Query Match 62.8%; Score 521.4; DB 22; Length 819;

Best Local Similarity 81.8%; Pred. No. 1.1e-137;

Matches 632; Conservative 0; Mismatches 126; Indels 15; Gaps 2;

QY 35 TTTTGGCGGGCGGGCGGCAATTCGCTTTTGGCGGGTTCAACTGCAGCAGCTCTGGGGCTG 94

Db 26 TCTTGGTAGCAACAGCTACAGGTGTCGACTCCAGGTCCAGCTGCAGCAGCTCTGGACCTG 85

QY 95 AGCTGTGAGGCGCTGGGGCTTCAGTGACGCTCTGCTGCAAGGCTTCGGGTACACATTTA 154

Db 86 ACTGTGAAAGCCTGGGGCTTCAGTGAAGATGTCTGCTGCAAGGCTTCTGGATACACCTTCG 145

XX 10-MAR-1999; 99JP-0063557.
XX (CHUS) CHUGAI SEIYAKU KK.
XX Fukushima N, Uno S;
XX WPI; 2000-587428/55.
XX P-PSDB; AAB23820.
XX Single stranded Fv antibody fragment inducing apoptosis in nucleated
PT blood cells having integrin associated protein for treatment of
PT leukemia
XX
XX Example 5; Page 66-68; 73pp; Japanese.
XX The present invention describes a polypeptide containing the variable
XX region of the light chain of a monoclonal antibody, which induces
XX apoptosis in nucleated blood cells having integrin associate protein
XX (IAP). Also described are: (1) DNA encoding the novel polypeptide;
XX (2) animal or microbial cells expressing the DNA of (1); and (3) agents
XX for the treatment of blood disorders which contain the polypeptide.
XX The polypeptide can be used in the treatment of blood disorders such
XX as leukemia. The present sequence encodes the protein sequence from
XX pCHOM2 NABL2-scFv, which is used in an example from the present
XX invention.
XX Sequence 819 BP; 207 A; 193 C; 219 G; 200 T; 0 other;
SQ

Query Match 62.6%; Score 519.8; DB 21; Length 819;
Best Local Similarity 81.6%; Pred. No. 3.2e-137;
Matches 631; Conservative 0; Mismatches 127; Indels 15; Gaps 2;
XX 35 TTTTGGGCGGGCGGCGCATCTCCCTTTGGCGGGTCAACTGCACGACTCTGGGCTG 94
DB 26 TCTTGGTAGCAACAGCTACAGGTGCGACTCCAGGCTCCAGCTGCACGACTGGAGCTG 85
XX 95 AGCTGGTGAGGCTTGGGGCTTCAGTGAGCTGTCTCTCAAGGCTTCGGGCTACACATTTA 154
DB 86 AACTGGTAAAGCTGGGGCTTCAGTGAAGTGTCTCGAAGGCTTCGTGATACACCTTCG 145
XX 155 CTGACTATGAATACACTGGGTGAGGAGACACCTGTGATGGCTGGAAATGGATTGGAG 214
DB 146 CTAACCATGTTATTCACTGGGTGAAGCAGAGCCAGGCGAGGCTTCAGTGGATTGGAT 205
XX 215 CTATTGATCTGAACTGGTGGTACTCCCTACATCAGAGTTCAAGGCAAGGCCATAG 274
DB 206 ATATTATCTTCAATGATGGTACTAAGTATATAGAAAGTTCAAGGCAAGGCCACTC 265
XX 275 TGACTGTAGACAAATCTCCAGCACAGCTACATGGAGCTCCGAGCTGACATCTGAAG 334
DB 266 TGACTTCAGACAAATCTCCACACAGCTTACATGGACCTCAGAGCTGGCTCTGAGG 325
XX 335 ACTCTGCGGTCTATTACTATACAGATGG-----TTTGAAGACTGGGGCCCAAG 382
DB 326 ACTCTGCGGTCTATTACTGTCAAGAGGGGTTACTATCTACGACACTGGGGCCCAAG 385
XX 383 GGACTCTGGTCACTGTCTCTGCA---CAGGTAATCCTCAGGATCTGGCTCCGAATCCA 439
DB 386 GCACCACTCTCACAGTCTCTCTAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 445
XX 440 AACCCGGGGATGTTGTGATGACCCCAACCACTCTCCCTGCTGTGAGTCTGGAGATC 499
DB 446 CGGATCGGATGTTGTGATGACCCCAAGTCCACTCTCCCTGCTGTGAGTCTGGAGATC 505
XX 500 AAGCTTCATCTCTTGAGATCTAGTCAGAGCCCTTTTACAGATTAATGGAATCACTATT 559
DB 506 AAGCTTCATCTCTTGAGATCAAGTCAGAGCCCTTTGTCACAGTAATGGAAGACCTATT 565
XX 560 TACATTGGTACCTGCAGAGCCAGGCGGCTCTCCAAAGCTCCTGATCTACAAAGTTTCCA 619
DB 566 TACATTGGTACCTGCAGAGCCAGGCGGCTCTCCAAAGCTCCTGATCTACAAAGTTTCCA 625

QY 620 ACCGATTTCTGGGGTCCAGACAGGTTTCAGTGGCAGTGGATCAGGGGACAGATTTTCACAC 679
DB 626 ACCGATTTCTGGGGTCCAGACAGGTTTCAGTGGCAGTGGATCAGTGCAGATTTTCACAC 685
QY 680 TCAAGATCAGCAGAGTGGAGGCTTGAGGATCTGGGAGTTTATTCTCTCTCAAGTACAC 739
DB 686 TCATGATCAGCAGAGTGGAGGCTTGAGGATCTGGGAGTTTATTCTCTCTCAAGTACAC 745
QY 740 ATGTTCCGTACAGTTTCGAGGGGGGACCAAGCTGCAATATAAAGAGAAAAA 792
DB 746 ATGTTCCGTACAGTTTCGAGGGGGGACCAAGCTGCAATATAAAGACTACAAA 798
RESULT 15
AAH78149
ID AAH78149 standard; DNA; 819 BP.
XX
XX AC AAH78149;
XX DT 26-NOV-2001 (first entry)
XX Nucleotide sequence of a murine antibody L chain.
DE
KW Apoptosis; nucleated blood cell; integrin-associated protein; IAP;
KW erythrocyte agglutination; blood disease; leukemia; myeloma;
KW Hodgkin's disease; non-Hodgkin's lymphoma; ss.
XX
XX Mus sp.
XX
XX Key Location/Qualifiers
FH CDS 1..816
FT /tag= a
FT /product= "L chain"
XX
XX WO200166737-A1.
XX
XX PD 13-SEP-2001.
XX
XX PF 12-MAR-2001; 2001WO-JP01912.
XX
XX PR 10-MAR-2000; 2000US-0523095.
XX PR 17-APR-2000; 2000JP-0115246.
XX PR 20-OCT-2000; 2000JP-0321822.
XX
XX PA (CHUS) CHUGAI SEIYAKU KK.
XX
XX PI Fukushima N, Tsuchiya M, Oh-eda M, Uno S, Kikuchi Y;
XX
XX DR WPI; 2001-570772/64.
XX
XX P-PSDB; AAG67496.
XX
XX PT Reconstituted polypeptide induces apoptosis in nucleated blood cells
XX that contain integrin-associated protein (IAP), is useful for the
XX treatment of blood diseases such as leukemia -
XX
XX Example 5; Page 115-117; 141pp; Japanese.
XX
XX PS The specification describes a reconstituted polypeptide, which
XX induces apoptosis in nucleated blood cells that contain
XX integrin-associated protein (IAP). The polypeptide binds to IAP
XX without causing agglutination of erythrocytes. The polypeptide
XX contains at least two H chain V domains and at least two L chain
XX V domains of a monoclonal antibody which induces apoptosis in
XX nuclear blood cells having IAP. The reconstituted polypeptide is used
XX for the treatment of blood diseases such as acute or chronic myeloid
XX leukemia, acute or chronic lymphoid leukemia, adult T-cell leukemia,
XX multiple myeloma, mixed leukemia, hairy cell leukemia, Hodgkin's
XX disease or non-Hodgkin's lymphoma. The present sequence encodes a
XX murine monoclonal antibody L chain, which is used in the course of
XX the invention.
XX
XX SQ Sequence 819 BP; 207 A; 193 C; 219 G; 200 T; 0 other;

```
Query Match      62.6%; Score 519.8; DB 22; Length 819;
Best Local Similarity 81.6%; Pred. No. 3.2e-137;
Matches 631; Conservative 0; Mismatches 127; Indels 15; Gaps 2;

QY 35 TTTTGGGGGGGGCGGCGCATTTCTGCCCTTTTGGGGGGTTCAACTGCAGCAGTCTCGGGCTG 94
   |||||
Db 26 TCTTGGTAGCAACAGCTACAGGTGTGACTCCAGGTCCAGCTGCAGCAGTCTGGACCTG 85
   |||||
QY 95 AGCTGGTAGGCGCTGGGGCTTCAGTGAGCGTGTCTGCAAGGCTTCGGGCTACACATTTA 154
   |||||
Db 86 AACTGGTAAAGCGCTGGGGCTTCAGTGAAGATGTCTGCAAGGCTTCTGGATACACCTTCG 145
   |||||
QY 155 CTGACTATGAATACACTGGGTGAGGCGAGCACCTGTGCATGGCCTGGAATGGATTGGAG 214
   |||||
Db 146 CTAACCAATGTTTCACTGGGTGAAGCAGAGCCAGGGCAGGCGCTTGAAGTGGATTGGAT 205
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QY 215 CTATTGATCTCGAAACTGGTGGTACTGCTCAATCAGAAAGTTCAAGGACAAGGCCATAG 274
   |||||
Db 206 ATATTATCTCTTACAATGATGGTACTAAGTATATAGAAAGTTCAAGGACAAGGCCACTC 265
   |||||
QY 275 TGACTGTAGACAAATCTCCAGCAGCAGCTACATGGAGCTCCGCGAGCCTGACATCTGAAG 334
   |||||
Db 266 TGACTTCAGACAAATCTCCACACAGCCTACATGGACCTCAGCAGCCTGGCCTCTGAGG 325
   |||||
QY 335 ACTCTGCCGTCTATTACTATACAGATGG- - - - -TTTGAGGACTGGGGCCCAAG 382
   |||||
Db 326 ACTCTGCCGTCTATTACTGTGCAAGAGGGGTTACTATCTTACGACGACTGGGGCCCAAG 385
   |||||
QY 383 GGACTCTGGTCACTGTCTCTGCA- - -GAGGGTAAATCTCAGGATCTGGCTCCGAAATCCA 439
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Db 386 GCACCACTCTCACAGTCTCTCAGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 445
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QY 440 AACCCGGGGATGTTGTGATGACCCCAACCACTCTCCCTGCGCTGTGAGTCTGGAGATC 499
   |||||
Db 446 GCGGATCGGATGTTGTGATGACCCCAAGTCCACTCTCCCTGCGCTGTGAGTCTGGAGATC 505
   |||||
QY 500 AAGCTCCATCTCTTGAGATCTAGTCAGAGCCTTTTACACAGTAAATGGAATCACCTATT 559
   |||||
Db 506 AAGCTCCATCTCTTGAGATCAAGTCAGAGCCTTGTGCACAGTAATGGAAGACCTATT 565
   |||||
QY 560 TACATTGGTACCTGCAGAGCCAGGCGCAGTCTCCAAAGTCTCCTGATCTACAAAGTTTCCA 619
   |||||
Db 566 TACATTGGTACCTGCAGAGCCAGGCGCAGTCTCCAAACTCTCCTGATCTACAAAGTTTCCA 625
   |||||
QY 620 ACCGATTTCTGGGGTCCCAAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTACAC 679
   |||||
Db 626 ACCGATTTCTGGGGTCCCAAGACAGGTTTCAGTGGCAGTGGATCAGTACAGATTTACAC 685
   |||||
QY 680 TCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGAGTTTATTCTGCTCTCAAGTACAC 739
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Db 686 TCATGATCAGCAGAGTGGAGGCTGAGGATCTGGAGTTTATTCTGCTCTCAAGTACAC 745
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QY 740 ATGTTCCGTACAGTTTCGGAGGGGGGACCAAGCTGGAAATAAAGAGAGAAAA 792
   |||||
Db 746 ATGTTCCGTACAGTTTCGGAGGGGGGACCAAGCTGGAAATAAAGACTACAA 798
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Job time : 185 secs

GenCore version 5.1.4.p5.4578
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DM protein - protein search, using sw model

Run on: May 16, 2003, 14:18:25 ; Search time 76 Seconds.
(without alignments)
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Title: US-09-358-321C-32

Perfect score: 1391

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Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	984.5	70.8	274	22	AA667495
5	984.5	70.8	274	23	ABG35313
6	984.5	70.8	274	23	AA647633
7	978.5	70.3	271	21	AA623820
8	978.5	70.3	271	22	AA667496
9	978.5	70.3	271	23	ABG35314
10	978.5	70.3	271	23	AA647634

11	973.5	70.0	533	22	AA667499	Amino acid sequenc
12	973.5	70.0	533	23	ABG35317	Thrombopoietin ago
13	973.5	70.0	533	23	AA647637	Murine MABL-2 #6.
14	963.5	69.3	274	21	AA623817	Plasmid pscM1 MABL
15	963.5	69.3	274	22	AA667493	Amino acid sequenc
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17	963.5	69.3	274	23	AA647631	Murine MABL-1 #3.
18	959.5	69.0	245	22	AA667498	Amino acid sequenc
19	959.5	69.0	245	23	ABG35316	Thrombopoietin ago
20	959.5	69.0	245	23	AA647636	Murine MABL-2 #5.
21	957.5	68.8	271	21	AA623818	Plasmid pCHOM1 MAB
22	957.5	68.8	271	22	AA667494	Amino acid sequenc
23	957.5	68.8	271	23	ABG35312	Thrombopoietin ago
24	957.5	68.8	271	23	AA647632	Murine MABL-1 #4.
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27	952	68.4	256	23	AA647638	Murine MABL-2 #7.
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29	943.5	67.8	251	20	AA617958	Mouse scfV fragmen
30	943.5	67.8	251	20	AA617962	Mouse scfV fragmen
31	943.5	67.8	507	23	AAU72858	8G7C10x4-7 bispeci
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33	943.5	67.8	510	23	AAU72860	Human p53 tetramer
34	927.5	66.7	252	17	AAW02279	26-10 anti-digoxin
35	927.5	66.7	252	19	AAW53169	26-10 anti-digoxin
36	927.5	66.7	252	20	AAW80423	Anti-digoxin srv
37	925.5	66.5	367	13	AA627244	Sequence encoded b
38	923.5	66.4	249	9	AA680154	Biosynthetic antib
39	922.5	66.3	246	13	AA627245	Sequence of the AA
40	914.5	65.7	311	11	AA605378	Multifunctional pr
41	914.5	65.7	313	22	AA662305	Single chain antib
42	910.5	65.5	246	14	AA644229	Chimeric Ig superf
43	906.5	65.2	311	9	AA680151	Multifunctional pr
44	890	64.0	251	22	AA670171	Recombinant antibo
45	889	63.9	261	14	AA644230	Chimeric Ig superf

ALIGNMENTS

RESULT 1

AA668992

ID AA668992 standard; Protein; 269 AA.

XX AA668992;

XX

DT 30-MAY-2000 (first entry)

DE Amino acid sequence of a single chain anti-delta9-desaturase antibody.

KW Delta9-desaturase; antibody; transit peptide; passenger protein;

KW plant cell organelle; maize; stearyl-ACP-delta9-desaturase;

KW transgenic plant.

XX Synthetic.

XX Mus sp.

XX

FT Key

FT Protein

FT Location/Qualifiers

FT 21..269

FT /note= "mature protein"

XX WO200005391-A1.

XX

PD 03-FEB-2000.

XX

PF 21-JUL-1999; 99WO-US16405.

XX

PR 21-JUL-1998; 98US-0093587.

XX

PA (DOWC) DOW AGROSCIENCES LLC.

XX

PI Sukhapinda K, Hasler JM, Petell JK, Strickland JA, Folkerts O;

XX


```

XX KW Monoclonal antibody; MABL; IAP; integrin associated protein;
XX KW single stranded Fv; apoptosis; blood disease; leukaemia;
XX KW cytostatic.
XX OS Mus sp.
XX WO200053634-A1.
XX PN
XX PD 14-SEP-2000.
XX PF 10-MAR-2000; 2000WO-JP01458.
XX PR 10-MAR-1999; 99JP-0063557.
XX PS (CHUS ) CHUGAI SEIYAKU KK.
XX PA Fukushima N, Uno S;
XX PI WPI; 2000-587428/55.
XX DR N-PSDB; AAA92443.
XX PT Single stranded Fv antibody fragment inducing apoptosis in nucleated
XX PT blood cells having integrin associated protein for treatment of
XX PT leukemia.
XX PS Example 5; Page 64-66; 73pp; Japanese.
XX CC The present invention describes a polypeptide containing the variable
XX CC region of the light chain of a monoclonal antibody, which induces
XX CC apoptosis in nucleated blood cells having integrin associate protein
XX CC (IAP). Also described are: (1) DNA encoding the novel polypeptide;
XX CC (2) animal or microbial cells expressing the DNA of (1); and (3) agents
XX CC for the treatment of blood disorders which contain the polypeptide.
XX CC The polypeptide can be used in the treatment of blood disorders such
XX CC as leukaemia. The present sequence represents the protein sequence from
XX CC pscM2 MABL2-scFv, which is used in an example from the present
XX CC invention.
XX SQ Sequence 274 AA;
Query Match 70.8%; Score 984.5; DB 21; Length 274;
Best Local Similarity 76.0%; Pred. NO. 1.1e-68;
Matches 196; Conservative 16; Mismatches 41; Indels 5; Gaps 2;
QY 10 LLAHAHSAFAAVALQOQSGAELVPGASVTLSCKASGYTFDTYEHVWVROTPTVHGLEWIG 69
DB 12 LLLAQAQPAQAQVLOQSGPELVPGASVKNKSCKASGYTFANHVHVKOKPGGLEWIG 71
QY 70 AIDPETGGTAYNOKFKDKAIVTVDKSSSTAYMELRSLTSEDSAVYYTR----WFDWQG 125
DB 72 YIYPNDGTKYNEKFKDKATLTSKSTTAYMDLSSLASEDSAVYYCARGYYTYDDWQG 131
QY 126 GTLVVTSABGKSSGSGSESKPG-DVWMTNPPLSLPVSGLGQASISCRSSSLHNSGITY 184
DB 132 GTTLTVSSGGGGGGGGGGGGGSDVWMTQSPSLPVSGLGQASISCRSSQSLVHNSGKTY 191
QY 185 LHWYLOKPGQSPKLLIYKVSNRFSGVDPDRFSGSGCTDFTLKISRVEAEDLGVYFCQSOT 244
DB 192 LHWYLOKPGQSPKLLIYKVSNRFSGVDPDRFSGSGSVTDFTLMTISRVEAEDLGVYFCQSOT 251
QY 245 HVPYTFGGGTGLEIKEEK 262
DB 252 HVPYTFGGGTGLEIKDYK 269
RESULT 4
AAG67495
ID AAG67495 standard; Protein; 274 AA.
XX AC AAG67495;
XX DT 26-NOV-2001 (first entry)

```

```

XX DE Amino acid sequence of a murine antibody L chain.
XX KW Apoptosis; nucleated blood cell; integrin-associated protein; IAP;
XX KW erythrocyte agglutination; blood disease; leukemia; myeloma;
XX KW Hodgkin's disease; non-Hodgkin's lymphoma.
XX OS Mus sp.
XX WO200166737-A1.
XX PN
XX PD 13-SEP-2001.
XX PF 12-MAR-2001; 2001WO-JP01912.
XX PR 10-MAR-2000; 2000US-0523095.
XX PR 17-APR-2000; 2000JP-0115246.
XX PR 20-OCT-2000; 2000JP-0321822.
XX PS (CHUS ) CHUGAI SEIYAKU KK.
XX PA Fukushima N, Tsuchiya M, Oh-eda M, Uno S, Kikuchi Y;
XX PI WPI; 2001-570772/64.
XX DR N-PSDB; AAH78148.
XX PT Reconstituted polypeptide induces apoptosis in nucleated blood cells
XX PT that contain integrin-associated protein (IAP), is useful for the
XX PT treatment of blood diseases such as leukemia.
XX PS Example 5; Page 113-115; 141pp; Japanese.
XX CC The specification describes a reconstituted polypeptide, which
XX CC induces apoptosis in nucleated blood cells that contain
XX CC integrin-associated protein (IAP). The polypeptide binds to IAP
XX CC without causing agglutination of erythrocytes. The polypeptide
XX CC contains at least two H chain V domains and at least two L chain
XX CC V domains of a monoclonal antibody which induces apoptosis in
XX CC nuclear blood cells having IAP. The reconstituted polypeptide is used
XX CC for the treatment of blood diseases such as acute or chronic myeloid
XX CC leukemia, acute or chronic lymphoid leukemia, adult T-cell leukemia,
XX CC multiple myeloma, mixed leukemia, hairy cell leukemia, Hodgkin's
XX CC disease or non-Hodgkin's lymphoma. The present sequence represents a
XX CC murine monoclonal antibody L chain, which is used in the course of
XX CC the invention.
XX SQ Sequence 274 AA;
Query Match 70.8%; Score 984.5; DB 22; Length 274;
Best Local Similarity 76.0%; Pred. NO. 1.1e-68;
Matches 196; Conservative 16; Mismatches 41; Indels 5; Gaps 2;
QY 10 LLAHAHSAFAAVALQOQSGAELVPGASVTLSCKASGYTFDTYEHVWVROTPTVHGLEWIG 69
DB 12 LLLAQAQPAQAQVLOQSGPELVPGASVKNKSCKASGYTFANHVHVKOKPGGLEWIG 71
QY 70 AIDPETGGTAYNOKFKDKAIVTVDKSSSTAYMELRSLTSEDSAVYYTR----WFDWQG 125
DB 72 YIYPNDGTKYNEKFKDKATLTSKSTTAYMDLSSLASEDSAVYYCARGYYTYDDWQG 131
QY 126 GTLVVTSABGKSSGSGSESKPG-DVWMTNPPLSLPVSGLGQASISCRSSSLHNSGITY 184
DB 132 GTTLTVSSGGGGGGGGGGGGGSDVWMTQSPSLPVSGLGQASISCRSSQSLVHNSGKTY 191
QY 185 LHWYLOKPGQSPKLLIYKVSNRFSGVDPDRFSGSGCTDFTLKISRVEAEDLGVYFCQSOT 244
DB 192 LHWYLOKPGQSPKLLIYKVSNRFSGVDPDRFSGSGSVTDFTLMTISRVEAEDLGVYFCQSOT 251
QY 245 HVPYTFGGGTGLEIKEEK 262
DB 252 HVPYTFGGGTGLEIKDYK 269

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RESULT 5
ABG35313
ID ABG35313 standard; Protein; 274 AA.
XX
XX ABG35313;
AC
XX
XX 30-JUL-2002 (first entry)
IDT
XX
XX Thrombopoietin agonist antibody associated protein #7.
DE
XX
XX Modified antibody; thrombopoietin; TPO; agonist;
XX
XX TPO receptor; platelet reduction-associated blood disease;
KW thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction.
XX
XX Mus sp.
XX
XX OS
XX
XX WO200233072-A1.
XX
XX 25-APR-2002.
PD
XX
XX 22-OCT-2001; 2001WO-JP09259.
XX
XX 20-OCT-2000; 2000JP-0321821.
XX
XX 17-APR-2001; 2001WO-JP03288.
XX
XX 12-SEP-2001; 2001JP-0277314.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Tsuchiya M, Ohtomo T, Yabuta N, Tsunoda H, Orita T;
PI
XX WPI; 2002-383513/41.
XX
XX N-PSDB; ABK71327.
XX
XX Degraded thrombopoietin agonist antibodies containing H and L chain V
XX domains of monoclonal antibody, useful in preventives and/or remedies
XX for blood diseases, thrombocytopenia following cancer chemotherapy or
XX leukaemia -
XX
XX Disclosure; Page 152-154; 213pp; Japanese.
XX
XX The invention describes a modified antibody comprising at least 2 heavy
XX chain variable domains and 2 or more light chain variable domains of an
XX antibody, and exhibits thrombopoietin (TPO) agonistic effect by causing
XX the TPO receptor to crosslink. The antibodies are useful in preventives
XX and/or remedies for platelet reduction-associated blood diseases,
XX thrombocytopenia following cancer chemotherapy or leukaemia. The
XX antibody can act as a TPO signal transduction agonist by transducing a
XX signal into cells by crosslinking a TPO receptor to exert TPO agonism.
XX This is the amino acid sequence of a thrombopoietin (TPO) agonist
XX antibody associated protein.
XX
XX Sequence 274 AA;
SQ
Query Match 70.8%; Score 984.5; DB 23; Length 274;
Best Local Similarity 76.0%; Pred. No. 1.1e-68;
Matches 196; Conservative 16; Mismatches 41; Indels 5; Gaps 2;
QY 10 LLAATAAFAAVALQOQSGAELVRPGASVTLSCKASGYTFTDYEIHWVROTVPVHGLEWIG 69
DB 12 LLLLAQAQPAWAQVQOQSGPELVKPGASVKMSCKASGYTFANHVIHWKQKPGQGLEWIG 71
QY 70 AIDPETGGTAYNOKFKDKAIVTVDKSSSTAYMELRLSTSDSAVYYTTR----WFDWQ 125
DB 72 YIYPNDGTKYNEKFKDKATLTSDKSSSTAYMDLSSLASDSAVYYCARGGYYTYDDWQ 131
QY 126 GTLVTVSAEGKSSGSGSEKPG-DVVMTPNPLSLPVLGDAQISCRSSQSLHNSGITY 184
DB 132 GTTLTVSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 191
QY 185 LHWYLOKPGOSPULLIYKYSNRFSGVDPDRFSGSGCTDFTLTKISRVEAEDLGVYFCQST 244
DB 192 LHWYLOKPGOSPULLIYKYSNRFSGVDPDRFSGSGVTDFTLTKISRVEAEDLGVYFCQST 251
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QY 245 HVPYTFGGGKLEIKEEK 262
DB 252 HVPYTFGGGKLEIKDYK 269

RESULT 6
AAM47633
ID AAM47633 standard; Protein; 274 AA.
XX
XX AAM47633;
AC
XX
XX 15-FEB-2002 (first entry)
DT
XX
XX Murine MABL-2 #3.
DE
XX
XX Murine; cytostatic; antiinflammatory; antianaemic; vasotropic;
KW antibody; signal transduction; cancer; inflammation; hormonal disorder;
XX leukaemia; lymphoma; aplastic anaemia; skeletal malformation.
XX
XX Mus sp.
XX
XX WO200179494-A1.
XX
XX 25-OCT-2001.
PD
XX
XX 17-APR-2001; 2001WO-JP03288.
XX
XX 17-APR-2000; 2000JP-0115246.
XX
XX 20-OCT-2000; 2000JP-0321821.
XX
XX 20-OCT-2000; 2000JP-0321822.
XX
XX 12-MAR-2001; 2001WO-JP01912.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Fukushima N, Tsuchiya M, Oheda M, Uno S, Kikuchi Y, Ohtomo T;
PI
XX WPI; 2002-066368/09.
XX
XX N-PSDB; ABA04524.
XX
XX Antibodies for treatment of diseases associated with cell
XX proliferation, hormonal disorders and cytokines comprise agonist
XX activity to signal transduction across cell membranes -
XX
XX Disclosure; Page 131-133; 173pp; Japanese.
XX
XX The present invention relates to modified antibodies. The antibodies
XX contain two or more H chain V domains and two or more L chain V domains
XX of a monoclonal antibody (Mab) which is capable of transmitting a signal
XX across the cell membrane by cross-linking a cell surface molecule, where
XX the antibodies can serve as signal transduction agonists. The antibodies
XX are useful for treatment and prevention of a broad range of disorders in
XX which signal transduction is implicated, such as cancer, inflammation,
XX hormonal disorders, leukaemia, malignant lymphoma, aplastic anaemia, and
XX skeletal malformations. The present sequence was used to illustrate the
XX present invention.
XX
XX Sequence 274 AA;
SQ
Query Match 70.8%; Score 984.5; DB 23; Length 274;
Best Local Similarity 76.0%; Pred. No. 1.1e-68;
Matches 196; Conservative 16; Mismatches 41; Indels 5; Gaps 2;
QY 10 LLAATAAFAAVALQOQSGAELVRPGASVTLSCKASGYTFTDYEIHWVROTVPVHGLEWIG 69
DB 12 LLLLAQAQPAWAQVQOQSGPELVKPGASVKMSCKASGYTFANHVIHWKQKPGQGLEWIG 71
QY 70 AIDPETGGTAYNOKFKDKAIVTVDKSSSTAYMELRLSTSDSAVYYTTR----WFDWQ 125
DB 72 YIYPNDGTKYNEKFKDKATLTSDKSSSTAYMDLSSLASDSAVYYCARGGYYTYDDWQ 131
QY 126 GTLVTVSAEGKSSGSGSEKPG-DVVMTPNPLSLPVLGDAQISCRSSQSLHNSGITY 184
DB 132 GTTLTVSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 191
QY 185 LHWYLOKPGOSPULLIYKYSNRFSGVDPDRFSGSGCTDFTLTKISRVEAEDLGVYFCQST 244
DB 192 LHWYLOKPGOSPULLIYKYSNRFSGVDPDRFSGSGVTDFTLTKISRVEAEDLGVYFCQST 251
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Qy	185	LHWYLOKPGOSP	KLLIYKYVNSR	FGS	GVDPDRF	SGSGSGT	DTFTL	KLISRVEA	EDLG	VYFC	QSQT	244
Db	192	LHWYLOKPGOSP	KLLIYKYVNSR	FGS	GVDPDRF	SGSGSGT	DTFTL	KLISRVEA	EDLG	VYFC	QSQT	251
Qy	245	HVPYTFGGGT	KLBIKEEK	262								
				:								
Db	252	HVPYTFGGGT	KLBIKDYG	269								
				:								

AA023820
ID AAB23820 standard; Protein; 271 AA.
XX
XX AAB23820;
XX
XX
DT 15-JAN-2001 (first entry)

XX DE Monoclonal antibody; MABU; IAP; integrin associated protein;
XX KW single stranded Fv; apoptosis; blood disease; leukaemia;
XX KW cytostatic.
XX CS
XX MU5 50

XX
FN WO200053634-A1.
XX
XX
PD 14-SEP-2000.
XX
XX 10-MAR-2000. 2000WO-TD01458
PF

10-MAR-1999; 99JP-0063557.
(CHUS) CHUGAI SEIVAKU KK.
Fukushima N. Uno S:

XX WPI; 2000-587428/55.
DR N-PSDB; AAA92444.
XX
PT Single stranded Fv antibody fragment inducing apoptosis in nucleated
PT blood cells having integrin associated protein for treatment of
PT leukemia -

xx The present invention describes a polypeptide containing the variable
ps region of the light chain of a monoclonal antibody, which induces
cc apoptosis in nucleated blood cells having integrin associate protein
cc

(2) animal or microbial cells expressing the DNA of (1); and (3) agents for the treatment of blood disorders which contain the polypeptide. The polypeptide can be used in the treatment of blood disorders such as leukaemia. The present sequence represents the protein sequence for pCHOM2 LAB2.2-scfv which is used in an example from the present

XX	Sequence	271 AA;	Query Match	70.3%	Score 978.5;	DB 21;	Length 271;
SQ			Best Local Similarity	74.0%;	Pred. NO. 3.2e-68;		
			Matches 196;	Conservative	19;	Mismatches 43;	Indels 7; Gaps

[illegible]

Qy	119	WFEDWGQGLTVTVAEGKSSGSGSESKPG-DVMTNPNPLSLPVSLGDQASISCRSSQSL	177
----	-----	--	-----

Db 4 SCILF--LVATATGVDVSOVLQOOSQGLVPCASVVKMSCKASGYTFANHVIHWKQPG 61
 QY 63 HGLEWICAIIDPETGCTAYNOKFKDKATVTDKSSSTAYMELRSITSEDSAVYYVTR---- 118
 Db 62 QGLEWIGYIIPYNDGTKYNEKFKDKATLTDKSSSTAYMOLSSLASDSAVYCARGGY 121
 QY 119 WFEDWGQGTTLVTSVSAEGKSSGSGSESKPG-DVVMTPNPLSLPVSLGQOASISCRSSQSL 177
 Db 122 TYDDWGQGTTLTVSSGGGGGGGGSDVVMTPQSPSLPVSLGQOASISCRSSQSLV 181
 QY 178 HSNGITLHWYLOKPGOSPKLLIYKVSNRFSVGPDRFSGSGSGTDTFLKISRVEAEDLGV 237
 Db 182 HSNKGTLYLHWYLOKPGOSPKLLIYKVSNRFSVGPDRFSGSGSVTDFTLMSRVEAEDLGV 241
 QY 238 YFCSQSTHVPYTFGGGKLEIKEEK 262
 Db 242 YFCSQSTHVPYTFGGGKLEIKEYK 266
 RESULT 9
 ABG35314
 ID ABG35314 standard; Protein; 271 AA.
 XX AC ABG35314;
 XX DT 30-JUL-2002 (first entry)
 XX Thrombopoietin agonist antibody associated protein #8.
 XX Modified antibody; thrombopoietin; TPO; agonist;
 KW TPO receptor; platelet reduction-associated blood disease;
 KW thrombocytopenia; cancer chemotherapy; leukaemia; signal transduction.
 XX OS Mus sp.
 XX PN WO200233072-A1.
 XX PD 25-APR-2002.
 XX PF 22-OCT-2001; 2001WO-JP09259.
 XX PR 20-OCT-2000; 2000JP-0321821.
 XX PR 17-APR-2001; 2001WO-JP03288.
 XX PR 12-SEP-2001; 2001JP-0277314.
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX TSuchiya M, Ohtomo T, Yabuta N, Tsunoda H, Orita T;
 XX WPI; 2002-383513/41.
 XX DR N-PSDB; ABK71328.
 XX Degraded thrombopoietin agonist antibodies containing H and L chain V
 PT domains of monoclonal antibody, useful in preventives and/or remedies
 PT for blood diseases, thrombocytopenia following cancer chemotherapy or
 PT leukaemia
 XX
 XX Disclosure; Page 154-156; 213pp; Japanese.
 XX The invention describes a modified antibody comprising at least 2 heavy
 CC chain variable domains and 2 or more light chain variable domains of an
 CC antibody, and exhibits thrombopoietin (TPO) agonistic effect by causing
 CC the TPO receptor to crosslink. The antibodies are useful in preventives
 CC and/or remedies for platelet reduction-associated blood diseases,
 CC thrombocytopenia following cancer chemotherapy or leukaemia. The
 CC antibody can act as a TPO signal transduction agonist by transducing a
 CC signal into cells by crosslinking a TPO receptor to exert TPO agonism.
 CC This is the amino acid sequence of a thrombopoietin (TPO) agonist
 CC antibody associated protein.
 XX
 XX Sequence 271 AA;
 SQ

Query Match

70.3%; Score 978.5; DB 23; Length 271;

Best Local Similarity 74.0%; Pred. No. 3.2e-68;
 Matches 196; Conservative 19; Mismatches 43; Indels 7; Gaps 3;
 QY 3 SAIVLVLLAAAHSAFAAVOLOOSGAELVRPCASVTLSCKASGYTFTDYEIHWVROTPV 62
 Db 4 SCILF--LVATATGVDVSOVLQOOSQGLVPCASVVKMSCKASGYTFANHVIHWKQPG 61
 QY 63 HGLEWICAIIDPETGCTAYNOKFKDKATVTDKSSSTAYMELRSITSEDSAVYYVTR---- 118
 Db 62 QGLEWIGYIIPYNDGTKYNEKFKDKATLTDKSSSTAYMOLSSLASDSAVYCARGGY 121
 QY 119 WFEDWGQGTTLVTSVSAEGKSSGSGSESKPG-DVVMTPNPLSLPVSLGQOASISCRSSQSL 177
 Db 122 TYDDWGQGTTLTVSSGGGGGGGGSDVVMTPQSPSLPVSLGQOASISCRSSQSLV 181
 QY 178 HSNGITLHWYLOKPGOSPKLLIYKVSNRFSVGPDRFSGSGSGTDTFLKISRVEAEDLGV 237
 Db 182 HSNKGTLYLHWYLOKPGOSPKLLIYKVSNRFSVGPDRFSGSGSVTDFTLMSRVEAEDLGV 241
 QY 238 YFCSQSTHVPYTFGGGKLEIKEEK 262
 Db 242 YFCSQSTHVPYTFGGGKLEIKEYK 266
 RESULT 10
 AAM47634
 ID AAM47634 standard; Protein; 271 AA.
 XX AC AAM47634;
 XX DT 15-FEB-2002 (first entry)
 XX Murine MABL-2 #4.
 XX Murine; cytostatic; antiinflammatory; antianaemic; vasotropic;
 KW antibody; signal transduction; cancer; inflammation; hormonal disorder;
 KW leukaemia; lymphoma; aplastic anaemia; skeletal malformation.
 XX OS Mus sp.
 XX PN WO200179494-A1.
 XX PD 25-OCT-2001.
 XX PF 17-APR-2001; 2001WO-JP03288.
 XX PR 17-APR-2000; 2000JP-0115246.
 XX PR 20-OCT-2000; 2000JP-0321821.
 XX PR 20-OCT-2000; 2000JP-0321822.
 XX PR 12-MAR-2001; 2001WO-JP01912.
 XX (CHUS) CHUGAI SEIYAKU KK.
 XX Fukushima N, Tsuchiya M, Oheda M, Uno S, Kikuchi Y, Ohtomo T;
 XX WPI; 2002-066368/09.
 XX DR N-PSDB; ABA04525.
 XX Antibodies for treatment of diseases associated with cell
 PT proliferation, hormonal disorders and cytokines comprise agonist
 PT activity to signal transmission across cell membranes -
 XX
 XX Disclosure; Page 133-135; 173pp; Japanese.
 CC The present invention relates to modified antibodies. The antibodies
 CC contain two or more H chain V domains and two or more L chain V domains
 CC of a monoclonal antibody (MAB) which is capable of transmitting a signal
 CC across the cell membrane by cross-linking a cell surface molecule, where
 CC the antibodies can serve as signal transmission agonists. The antibodies
 CC are useful for treatment and prevention of a broad range of disorders in
 CC which signal transmission is implicated, such as cancer, inflammation, and
 CC hormonal disorders, leukaemia, malignant lymphoma, aplastic anaemia, and
 CC skeletal malformations. The present sequence was used to illustrate the

[illegible]

```

XX WPI: 2000-587428/55.
XX N-PSDB; AAA92439.
XX Single stranded Fv antibody fragment inducing apoptosis in nucleated
XX blood cells having integrin associated protein for treatment of
XX leukemia.
XX Example 5; Page 59-61; 73pp; Japanese.
XX The present invention describes a polypeptide containing the variable
XX region of the light chain of a monoclonal antibody, which induces
XX apoptosis in nucleated blood cells having integrin associated protein
XX (IAP). Also described are: (1) DNA encoding the novel polypeptide;
XX (2) animal or microbial cells expressing the DNA of (1); and (3) agents
XX for the treatment of blood disorders which contain the polypeptide.
XX The polypeptide can be used in the treatment of blood disorders such
XX as leukemia. The present sequence represents the protein sequence from
XX pscM1 MABU1-scfv, which is used in an example from the present
XX invention.
XX Sequence 274 AA;
XX
Query Match 69.3%; Score 963.5; DB 21; Length 274;
Best Local Similarity 74.8%; Pred. No. 4.7e-67;
Matches 193; Conservative 15; Mismatches 45; Indels 5; Gaps 2;

QY 10 LLAASAHSAFAAALQOQSGAELVRPGASVTLSCKASGYTFTDYBIHWVRQTPVHGLEWIG 69
DB 12 LLLAQAQPAQAQVQLQOQSGDPLVKPGASVKMSCKASGYTFVNHVHWKQKPGOGLEWIG 71
QY 70 AIDPETGGTAYNQKFKDKAIVTVDKSSSTAYMELRLSSTSDSAVYYTRW----FEDWGQ 125
DB 72 YIYPYNDGTQYNEKFKGKATLTSEKSSAAAYMELSLASEDSAVYYCARGGYYSYDDWGQ 131
QY 126 GTLVTVAEGKSGSGSESKPG-DVWMTNPPLSLPVSILGDOASTSCRSSOSLLHSGNTY 184
DB 132 GTTUTVSSGGGGGGGGGGGGSDVWMTQTPLSLPVSILGDOASTSCRSSOSLLHSGNTY 191
QY 185 LHWYLOKPGQSPKLLIYKVNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCQSQT 244
DB 192 LQWYLOKPGQSPKLLIYKVNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCQSQT 251
QY 245 HVPYTFGGGKLEIKEEK 262
DB 252 HVPYTSGGGKLEIKDYK 269

RESULT 15
AAG67493
ID AAG67493 standard; Protein; 274 AA.
AC AAG67493;
XX
DT 26-NOV-2001 (first entry)
XX
DE Amino acid sequence of a murine antibody L chain.
XX
KW Apoptosis; nucleated blood cell; integrin-associated protein; IAP;
KW erythrocyte agglutination; blood disease; leukemia; myeloma;
KW Hodgkin's disease; non-Hodgkin's lymphoma.
XX
OS Mus sp.
XX
PN WO200166737-A1.
XX
PD 13-SEP-2001.
XX
PF 12-MAR-2001; 2001WO-JF01912.
XX
PR 10-MAR-2000; 2000US-0523095.
PR 17-APR-2000; 2000JP-0115246.
PR 20-OCT-2000; 2000JP-0321822.

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XX (CHUS ) CHUGAI SEIYAKU KK.
XX Fukushima N, Tsuchiya M, Oh-eda M, Uno S, Kikuchi Y;
XX WPI: 2001-570772/64.
XX N-PSDB; AAH78144.
XX Reconstituted polypeptide induces apoptosis in nucleated blood cells
XX that contain integrin-associated protein (IAP), is useful for the
XX treatment of blood diseases such as leukemia.
XX Example 5; Page 108-110; 141pp; Japanese.
XX The specification describes a reconstituted polypeptide, which
XX induces apoptosis in nucleated blood cells that contain
XX integrin-associated protein (IAP). The polypeptide binds to IAP
XX without causing agglutination of erythrocytes. The polypeptide
XX contains at least two H chain V domains and at least two L chain
XX V domains of a monoclonal antibody which induces apoptosis in
XX nuclear blood cells having IAP. The reconstituted polypeptide is used
XX for the treatment of blood diseases such as acute or chronic myeloid
XX leukemia, acute or chronic lymphoid leukemia, adult T-cell leukemia,
XX multiple myeloma, mixed leukemia, hairy cell leukemia, Hodgkin's
XX disease or non-Hodgkin's lymphoma. The present sequence represents a
XX a murine monoclonal antibody L chain, which is used in the course of
XX the invention.
XX Sequence 274 AA;
XX
Query Match 69.3%; Score 963.5; DB 22; Length 274;
Best Local Similarity 74.8%; Pred. No. 4.7e-67;
Matches 193; Conservative 15; Mismatches 45; Indels 5; Gaps 2;

QY 10 LLAASAHSAFAAALQOQSGAELVRPGASVTLSCKASGYTFTDYBIHWVRQTPVHGLEWIG 69
DB 12 LLLAQAQPAQAQVQLQOQSGDPLVKPGASVKMSCKASGYTFVNHVHWKQKPGOGLEWIG 71
QY 70 AIDPETGGTAYNQKFKDKAIVTVDKSSSTAYMELRLSSTSDSAVYYTRW----FEDWGQ 125
DB 72 YIYPYNDGTQYNEKFKGKATLTSEKSSAAAYMELSLASEDSAVYYCARGGYYSYDDWGQ 131
QY 126 GTLVTVAEGKSGSGSESKPG-DVWMTNPPLSLPVSILGDOASTSCRSSOSLLHSGNTY 184
DB 132 GTTUTVSSGGGGGGGGGGGGSDVWMTQTPLSLPVSILGDOASTSCRSSOSLLHSGNTY 191
QY 185 LHWYLOKPGQSPKLLIYKVNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCQSQT 244
DB 192 LQWYLOKPGQSPKLLIYKVNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCQSQT 251
QY 245 HVPYTFGGGKLEIKEEK 262
DB 252 HVPYTSGGGKLEIKDYK 269

Search completed: May 16, 2003, 14:23:52
Job time : 79 secs

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

QOM nucleic - nucleic search, using sw model

Run on: May 16, 2003, 18:44:54 ; Search time 1122 Seconds
(without alignments)
11980.619 Million cell updates/sec

Title: US-09-358-321C-31

Perfect score: 830

Sequence: 1 ttgtaaatggaagcgtat.....ctgaattagtaagcgccgc 830

Scoring table: IDENTITY_NUC

Gapop 10.0 , Capext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthm:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: gb_gss:*

18: em_gss_hum:*

19: em_gss_inv:*

20: em_gss_pln:*

21: em_gss_vrt:*

22: em_gss_fun:*

23: em_gss_mam:*

24: em_gss_mus:*

25: em_gss_other:*

26: em_gss_pro:*

27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	317.6	38.3	926	14	BQ959057
2	316	38.1	678	13	BQ962941
3	316	38.1	925	13	BQ963141
4	314.4	37.9	997	13	B1107100
5	312.2	37.6	962	12	BF578262
6	309.2	37.3	793	10	BE307894
					601096348

7	308	37.1	693	13	BQ964281	BQ964281
8	302.2	36.4	716	13	BQ964192	BQ964192
9	300.2	36.2	743	13	BQ968770	BQ968770
10	296.6	35.7	965	12	BF577927	BF577927
11	293.6	35.4	913	14	BQ933319	BQ933319
12	280.8	33.8	509	17	A2791472	A2791472
13	279.6	33.7	898	12	BF135785	BF135785
14	278.2	33.5	755	13	B1109046	B1109046
15	277.8	33.5	884	13	BQ963735	BQ963735
16	276.6	33.3	772	10	BE285427	BE285427
17	276.4	33.3	707	13	BE250555	BE250555
18	262.2	31.6	1018	14	BQ934943	BQ934943
19	247	29.8	766	13	BQ969524	BQ969524
20	240.6	29.0	512	12	BF023434	BF023434
21	240	28.9	723	13	BQ969577	BQ969577
22	240	28.9	952	12	BQ758592	BQ758592
23	236.6	28.5	995	14	BQ712430	BQ712430
24	236.4	28.5	1576	11	AK007918	AK007918
25	235.2	28.3	898	14	BQ708918	BQ708918
26	235.2	28.3	960	14	BQ711007	BQ711007
27	234.8	28.3	640	14	BQ109114	BQ109114
28	233.6	28.1	471	10	AW405772	AW405772
29	232	28.0	614	10	AW405187	AW405187
30	230.2	27.7	634	14	BM783161	BM783161
31	228.6	27.5	454	10	AW408883	AW408883
32	228	27.5	909	13	B1105366	B1105366
33	227.2	27.4	896	13	BQ963760	BQ963760
34	227	27.3	967	13	BQ964352	BQ964352
35	226	27.2	491	12	BF174573	BF174573
36	225.4	27.2	522	13	BM511309	BM511309
37	225.4	27.2	751	12	BQ542438	BQ542438
38	224.4	27.0	598	13	B1104341	B1104341
39	224.4	27.0	829	12	BF144014	BF144014
40	224	27.0	696	13	B1838136	B1838136
41	223.8	27.0	363	9	AA464313	AA464313
42	223.8	27.0	488	10	AW405725	AW405725
43	223.8	27.0	990	13	BF838327	BF838327
44	223.6	26.9	739	10	BE284158	BE284158
45	223.4	26.9	488	14	H25625	H25625

ALIGNMENTS

RESULT 1
BQ959057
LOCUS
DEFINITION AGENCOURT_10049748 NCI_CGAP_Co24 Mus musculus cDNA clone
IMAGE:6479377 5', mRNA sequence.
ACCESSION BQ959057
VERSION BQ959057.1 GI:22374535
KEYWORDS EST.
SOURCE house mouse
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contract: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov

Tissue Procurement: The Cepko Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14024 row: h column: 02
High quality sequence stop: 692.
Location/Qualifiers
1. 926

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/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:6479377"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      237 a      251 c      235 t      1 others
ORIGIN
Query Match      38.3%; Score 317.6; DB 14; Length 926;
Best Local Similarity 95.9%; Pred. No. 7 le-85;
Matches 326; Conservative 0; Mismatches 14; Indels 0; Gaps 0;
QY 444 CCGGGATGTTGATGACCCCAACCACTCTCCCTGCTGTCAGTCTTTGGAGATCAAGC 503
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 86 CAGTGATGTTGATGACCCCAAGCTCCACTCTCCCTGCTGTCAGTCTTTGGAGATCAAGC 145
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 504 CTCATCTCTTGAGATCTAGTCAGAGCCCTTTTACACAGTAATGGAATCACCTATTATTA 563
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 146 CTCATCTCTTGAGATCTAGTCAGAGCCCTTTTACACAAATAATGGAACACCACTATTATTA 205
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 564 TTGGTACCTGCAGAACCCAGGCGCAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCG 623
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 206 TTGGTACCTGCAGAACCCAGGCGCAGTCTCCAAAGCTCTGATCTACAAAGTTTCTAACCG 265
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 624 ATTTTCTGGGTCCTCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTACACTCAA 683
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 266 ATTTTCTGGGTCCTCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTACACTCAA 325
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 684 GATCAGACAGTGGAGCTCAGATCTGGAGTTTATTTCTGCTCTCAAGTACACATGT 743
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 326 GATCAGACAGTGGAGCTCAGATCTGGAGTTTATTTCTGCTCTCAAGTACACATAT 385
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 744 TCCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAAA 783
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 386 TCCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAAA 425
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 2
LOCUS      BG962941      678 bp      mRNA      linear      EST 12-JUN-2001
DEFINITION 602827925F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4982670 5',
            mRNA sequence.
ACCESSION  BG962941
VERSION    BG962941.1 GI:14350578
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 678)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10986 row: a column: 07
            High quality sequence stop: 676.
            Location/Qualifiers
            1..678
            /organism="Mus musculus"
            /strain="FVB/N"

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/clone="taxon:10090"
/clone="IMAGE:4982670"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT      181 a      173 c      158 g      166 t
ORIGIN
Query Match      38.1%; Score 316; DB 13; Length 678;
Best Local Similarity 95.6%; Pred. No. 2e-84;
Matches 325; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 444 CCGGGATGTTGATGACCCCAACCACTCTCCCTGCTGTCAGTCTTTGGAGATCAAGC 503
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 74 CAGTGATGTTGATGACCCCAAACTCCACTCTCCCTGCTGTCAGTCTTTGGAGATCAAGC 133
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 504 CTCATCTCTTGAGATCTAGTCAGAGCCCTTTTACACAGTAATGGAATCACCTATTATTA 563
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 134 CTCATCTCTTGAGATCTAGTCAGAGCCCTTTTACACAGTAATGGAACACCACTATTATTA 193
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 564 TTGGTACCTGCAGAACCCAGGCGCAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCG 623
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 194 TTGGTACCTGCAGAACCCAGGCGCAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCG 253
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 624 ATTTTCTGGGTCCTCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTACACTCAA 683
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 254 ATTTTCTGGGTCCTCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTACACTCAA 313
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 684 GATCAGACAGTGGAGCTCAGATCTGGAGTTTATTTCTGCTCTCAAGTACACATGT 743
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 314 GATCAGACAGTGGAGCTCAGATCTGGAGTTTATTTCTGCTCTCAAGTACACATGT 373
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 744 TCCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAAA 783
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 374 TCCATTACGTTCCGCTCGGGACAAAGTTGGAATAAAAA 413
Db      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3
LOCUS      BG963141      925 bp      mRNA      linear      EST 12-JUN-2001
DEFINITION 602828165F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4982705 5',
            mRNA sequence.
ACCESSION  BG963141
VERSION    BG963141.1 GI:14350778
KEYWORDS   EST.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 925)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Tissue Procurement: Jeffrey E. Green, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10986 row: b column: 18
            High quality sequence stop: 729.
            Location/Qualifiers
            1..925
            /organism="Mus musculus"
            /strain="FVB/N"
            /db_xref="taxon:10090"
            /clone="IMAGE:4982705"

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/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (fl-phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 245 a 246 c 206 g 228 t
ORIGIN

Query Match 38.1%; Score 316; DB 13; Length 925;
Best Local Similarity 95.6%; Pred. No. 2.2e-84;
Matches 325; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 444 CGGGGATGTTGTGATGACCCCAACCCACTCTCCCTCCCTGCTGAGTTTGGAGATCAAGC 503
DB 75 CAGTGATGTTGTGATGACCCCAACCCACTCTCCCTCCCTGCTGAGTTTGGAGATCAAGC 134
QY 504 CTCCATCTCTTGAGATCTAGTCAGAGCCITTTACACAGTAATGGAATCACTATTATACA 563
DB 135 CTCCATCTCTTGAGATCTAGTCAGAGCCITTTACACAGTAATGGAATCACTATTATACA 194
QY 564 TTGTTACTCTGAGAAGCCAGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAACCG 623
DB 195 TTGTTACTCTGAGAAGCCAGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAACCG 254
QY 624 ATTTCTGGGGTCCACACAGGTTTCAGTGGCAGTGGATCAGGACACATTTCACTCAA 683
DB 255 ATTTCTGGGGTCCACACAGGTTTCAGTGGCAGTGGATCAGGACACATTTCACTCAA 314
QY 684 GATCAGCAGAGTGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGT 743
DB 315 GATCAGCAGAGTGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGT 374
QY 744 TCCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAAA 783
DB 375 TCCATTACGTTCCGTCGGGACAAAGTTTGGAAATAAAAA 414

RESULT 4
BI107100
LOCUS 602894523F1 NCI_CGAP_Lu29 997 bp mRNA linear EST 26-JUN-2001
DEFINITION mRNA sequence.
ACCESSION BI107100
VERSION BI107100.1 GI:14557993
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 997)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1109 row: m column: 05
High quality sequence stop: 832.
Location/Qualifiers
1..997
/organism="Mus musculus"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:5039788"
/clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary."

FEATURES
source

Stem cell origin."
/lab_host="DH10B"
/notes="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dr.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

BASE COUNT 270 a 272 c 213 g 242 t
ORIGIN

Query Match 37.9%; Score 314.4; DB 13; Length 997;
Best Local Similarity 95.3%; Pred. No. 6.8e-84;
Matches 324; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 444 CGGGGATGTTGTGATGACCCCAACCCACTCTCCCTCCCTGCTGAGTTTGGAGATCAAGC 503
DB 83 CAGTGATGTTGTGATGACCCCAACCCACTCTCCCTCCCTGCTGAGTTTGGAGATCAAGC 142
QY 504 CTCCATCTCTTGAGATCTAGTCAGAGCCITTTACACAGTAATGGAATCACTATTATACA 563
DB 143 CTCCATCTCTTGAGATCTAGTCAGAGCCITTTACACAGTAATGGAATCACTATTATACA 202
QY 564 TTGTTACTCTGAGAAGCCAGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAACCG 623
DB 203 TTGTTACTCTGAGAAGCCAGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAACCG 262
QY 624 ATTTCTGGGGTCCACACAGGTTTCAGTGGCAGTGGATCAGGACACATTTCACTCAA 683
DB 263 ATTTCTGGGGTCCACACAGGTTTCAGTGGCAGTGGATCAGGACACATTTCACTCAA 322
QY 684 GATCAGCAGAGTGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGT 743
DB 323 GATCAGCAGAGTGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGT 382
QY 744 TCCGTACACGTTCCGAGGGGGACCAAGCTGGAATAAAAA 783
DB 383 TCCGTATACGTTCCGATCGGGGACCAAGCTGGAATAAAAA 422

RESULT 5
BF578262
LOCUS 602093093F1 NCI_CGAP_Co24 962 bp mRNA linear EST 12-DEC-2000
DEFINITION mRNA sequence.
ACCESSION BF578262
VERSION BF578262.1 GI:11651974
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 962)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9770 row: i column: 23
High quality sequence stop: 681.
Location/Qualifiers
1..962
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4207582"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (fl-phage-resistant)"

FEATURES
source

/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.6 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT 262 a 253 c 221 g 226 t
ORIGIN

Query Match 37.6%; Score 312.2; DB 12; Length 962;
Best Local Similarity 94.7%; Pred. No. 3.1e-83;
Matches 323; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 443 CCGGGATGTTGATGACCCCAAAACCACTCTCCCTGCTGTGCTGAGTCTGGAGATCAAG 502
DB 85 CCAATGATGTTGATGACCCCAAACTCCACTCTCCCTGCTGTGCTGAGTCTGGAGATCAAG 144
QY 503 CTCCATCTCTTCGAGATCTAGTCAGAGCCCTTTTACACAGCTTAATGAATCAACCTATTATAC 562
DB 145 CTCCATCTCTTCGAGATCTAGTCAGAGCCCTTTTACACAGCTTAATGAATCAACCTATTATAC 204
QY 563 ATTGGTACCTGCAGAACCCAGGCCAGCTCTCAAAGCTCTCTGATCTACAAAGTTTCCAAAC 622
DB 205 ATTGGTACCTGCAGAACCCAGGCCAGCTCTCAAAGCTCTCTGATCTGCAAACTTTCCAAAC 264
QY 623 GATTTCTGGGGTCCAGACAGAGTTTCAAGTGGAGTGTAGTCAGGACAGATTTACACTCA 682
DB 265 GATTTCTGGGGTCCAGACAGAGTTTCAAGTGGAGTGTAGTCAGGACAGATTTACACTCA 324
QY 683 AGATCAGCAGAGTGGAGGCTGAGGATCTGGAGTTTATTTCTGCTCTCAAAGTACACATG 742
DB 325 AGATCAGCAGAGTGGAGGCTGAGGATCTGGAGTTTATTTCTGCTCTCAAAGTACACATA 384
QY 743 TTCGTACAGTTTCGGAGGGGGACCAAGCTCGAAATAAAA 783
DB 385 TTCCATTACAGTTTCGGCTCGGGGACCAAGTTGGAATAAAA 425

RESULT 6
BE307894 793 bp mRNA linear EST 26-OCT-2000
LOCUS 601096548F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3491195 5',
DEFINITION mRNA sequence.
ACCESSION BE307894
VERSION BE307894.1 GI:9163704
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 793)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8534 row: p column: 12
High quality sequence stop: 514.
Location/Qualifiers
1. .793
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3491195"
/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"

FEATURES
source

1. .793
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3491195"
/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"

/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

BASE COUNT 156 a 210 c 217 g 210 t
ORIGIN

Query Match 37.3%; Score 309.2; DB 10; Length 793;
Best Local Similarity 94.7%; Pred. No. 2.4e-82;
Matches 320; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 446 GGGATGTTGATGACCCCAAAACCACTCTCCCTGCTGTGCTGAGTCTGGAGATCAAGCCT 505
DB 80 GTGATGTTGATGACCCCAAACTCTCCCTGCTGTGCTGAGTCTGGAGATCAAGCCT 139
QY 506 CCATCTCTTCGAGATCTAGTCAGAGCCCTTTTACACAGTAAATGAATCACTATTACATT 565
DB 140 CCATCTCTTCGAGATCTAGTCAGAGCCCTTTTACACAGTAAATGAATCACTATTACATT 199
QY 566 GGTACTCTGCAGAACCCAGGCCAGCTCTCAAAGCTCTGATCTACAAAGTTTCCAAACCGAT 625
DB 200 GGTCTCTGCAGAACCCAGGCCAGCTCTCAAAGCTCTGATCTACAAAGTTTCCAAACCGAT 259
QY 626 TTTCTGGGTCTCCAGACAGGTTTCAAGTGGAGTGGATCAGGACAGATTTTCACTCAAGA 685
DB 260 TTTCTGGGTCTCCAGACAGGTTTCAAGTGGAGTGGATCAGGACAGATTTTCACTCAAGA 319
QY 686 TCAGCAGATCGAGCTGAGGATCTGGAGTTTATTTCTGCTCTCAAAGTACACATGTTTC 745
DB 320 TCACCAGATGGAGGCTGAGGATCTGGAGTTTATTTCTGCTCTCAAAGTACACATGTTTC 379
QY 746 CGTACACGTTTCGGAGGGGGACCAAGCTCGAAATAAAA 783
DB 380 CGCTACGTTTCGGTCTGGGACCAAGCTGGAGCTGAAA 417

RESULT 7
BG964281 693 bp mRNA linear EST 12-JUN-2001
LOCUS 602829076F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4983618 5',
DEFINITION mRNA sequence.
ACCESSION BG964281
VERSION BG964281.1 GI:14351918
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 693)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10988 row: h column: 19
High quality sequence stop: 553.
Location/Qualifiers
1. .693
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4983618"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;

FEATURES
source

1. .693
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4983618"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;

Site 2: Sali; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI CGAP Library."

BASE COUNT 179 a 184 c 160 g 169 t

ORIGIN

Query Match 37.1%; Score 308; DB 13; Length 693;
Best Local Similarity 94.1%; Pred. No. 5.4e-8;
Matches 320; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 444 CGGGGATGTTCTGATGACCCCAACCCACTCTCCCTGCTGTGAGTCTTGAGATCAAGC 503
DB 89 CAGTGATGTTGTTGACCCAACTCCACTCTCCCTGCTGTGAGTCTTGAGATCAAGC 148
QY 504 CTCATCTCTTTCAGATCTAGTCAGAGCCTTTTACACAGTAATGAATCACTATTAC 563
DB 149 CTCATCTCTTTCAGATCTAGTCAGAGCCTTTTACACAGTAATGAATCACTATTAC 208
QY 564 TTGTACTCTGAGAACCCAGCCAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAACCG 623
DB 209 TTGTACTCTGAGAACCCAGCCAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAACCG 268
QY 624 ATTTCTGGGTCCTCAGACAGTTCAGTGGCAGTGGATCAGGACAGATTTCACTCAA 683
DB 269 ATTTCTGGGTCCTCAGACAGTTCAGTGGCAGTGGATCAGGACAGATTTCACTCAA 328
QY 684 GATCAGCAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGT 743
DB 329 GATCAGCAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGT 388
QY 744 TCCGTACAGTTCGGAGGGGACCAAGCTGGAATAAAA 783
DB 389 TCCGTGACGTTCCGTGGAGGCCACCAACTGGAAATCAA 428

RESULT 8
BG964192
LOCUS 602828968F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4983617 5',
DEFINITION mRNA sequence.

ACCESSION BG964192
VERSION BG964192.1 GI:14351829
KEYWORDS EST.

SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 716)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: L1AM10988 row: h column: 18
High quality sequence stop: 716.

FEATURES
source
1..716
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4983617"
/lab_host="NCI CGAP Co24"

/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1: NotI;
Average insert size 1.6 kb. Constructed by Life

Technologies. Note: this is a NCI CGAP Library."

BASE COUNT 179 a 184 c 160 g 169 t

Technologies. Note: this is a NCI CGAP Library."

BASE COUNT 191 a 188 c 163 g 174 t

ORIGIN

Query Match 36.4%; Score 302.2; DB 13; Length 716;
Best Local Similarity 94.6%; Pred. No. 3.1e-80;
Matches 313; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 453 TGTGTGATGACCCCAACCCACTCTCCCTGCTGTGAGTCTTGAGATCAAGCTCCATCTC 512
DB 97 TGTGTGATGACCCCAACCCACTCTCCCTGCTGTGAGTCTTGAGATCAAGCTCCATCTC 156
QY 513 TTCCAGATCTAGTCAGAGCCTTTTACACAGTAATGAATCACTATTACATTTGTTACCT 572
DB 157 TTCCAGATCTAGTCAGAGCCTTTTACACAGTAATGAATCACTATTACATTTGTTACCT 216
QY 573 GCAGAGCCAGGCGGAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAACCGATTTCTGG 632
DB 217 GCAGAGCCAGGCGGAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAACCGATTTCTGG 276
QY 633 GGTCCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTCACTCAAGATCAGCAG 692
DB 277 GGTCCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTCACTCAAGATCAGCAG 336
QY 693 AGTGGAGGCTGAGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGTTCCGTACAC 752
DB 337 AGTGGAGGCTGAGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGTTCCGTGAC 396
QY 753 GTTCGGAGGGGGACCAAGCTGGAATAAAA 783
DB 397 GTTCGGAGGGGGACCAAGCTGGAATAAAA 427

RESULT 9
BG968770
LOCUS 602836677F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4990962 5',
DEFINITION mRNA sequence.

ACCESSION BG968770
VERSION BG968770.1 GI:14356407
KEYWORDS EST.

SOURCE house mouse.
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 743)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: L1AM11007 row: j column: 19
High quality sequence stop: 659.

FEATURES
source
1..743
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:4990962"
/lab_host="NCI CGAP Co24"

/note="Organ: colon; Vector: pCMV-SPORT6; Site: 1: NotI;
Average insert size 1.6 kb. Constructed by Life

Technologies. Note: this is a NCI CGAP Library."

BASE COUNT 199 a 196 c 181 g 167 t

ORIGIN

Query Match 36.2%; Score 300.2; DB 13; Length 743;
 Best Local Similarity 94.4%; Pred. No. 1.3e-79;
 Matches 322; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

QY 444 CGGGGATGTTGTGATGACCCCAACCCCACTCTCCCTGCCCTGTGAGTCTTGGAGATCAAGC 503
 DB 68 CAGTGATGTTGTGATGACCCCAACTCCACTCTCCCTGCCCTGTGAGTCTTGGAGATCAAGC 127
 QY 504 CTCATCTCTTGAGATCTAGTCAGAGCCCTTTTACACAGTAATGGAATCACTATTATACA 563
 DB 128 CTCATCTCTTGAGATCTAGTCAGAGCCCTTTTACACAGTAATGGAATCACTATTATACA 187
 QY 564 TTGTACTCTCAGAAAGCCAGCCAGTCTCCAAAGCTCCTCATCTACAAAGTTTCCAAACCG 623
 DB 188 TTGTACTCTCAGAAAGCCAGCCAGTCTCCAAAGCTCCTCATCTACAAAGTTTCCAAACCG 247
 QY 624 ATTTCTGGGGTCCCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTCACTCAA 683
 DB 248 ATTTCTGGGGTCCCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTCACTCAA 307
 QY 684 GATCA-CCAGAGTGGAGCTGAGGATCTGGAGTTTATTCTGCTCTCAAAGTACACATG 742
 DB 308 GATCAGCTAGAGTGGAGCTGAGGATCTGGAGTTTATTCTGCTCTCAAAGTACACATG 367
 QY 743 TTCGCTACAGTTTCGGAGGGGGACCAAGCTGGAATAAAAA 783
 DB 368 TTCGCTACAGTTTCGGAGGGGGACCAAGCTGGAAGTGAAG 408

RESULT 10

BF577927
 LOCUS 602091947F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4206515 5',
 DEFINITION mRNA sequence.
 ACCESSION BF577927
 VERSION BF577927.1 GI:11651639
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 965)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Jeffrey E. Green, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LAM9767 row: m column: 12
 High quality sequence stop: 665.
 Location/Qualifiers
 1..965
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:4206515"
 /clone_lib="NCI_CGAP_Co24"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.6 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT

ORIGIN

269 a 241 c 242 g 213 t

Query Match

Best Local Similarity 95.5%; Score 296.6; DB 12; Length 965;
 Matches 316; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

QY 453 TGTGATGACCCCAACCCCACTCTCCCTGCCCTGTGAGTCTTGGAGATCAAGCTCCATCTC 512
 DB 92 TGTGATGACCCCAACCCCACTCTCCCTGCCCTGTGAGTCTTGGAGATCAAGCTCCATCTC 151
 QY 513 TTGCAGATCTAGTCAGAGCCCTTTTACACAGTAATGGAATCACTATTATACATTGGTACCT 572
 DB 152 TTGCAGATCTAGTCAGAGCCCTGTGATCAGTAATGGAACACCTATTATACA-TGGTACCT 210
 QY 573 GCAGAAGCCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAAACCGATTCTCG 632
 DB 211 GCAGAAGCCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAAACCGATTCTCG 270
 QY 633 GTTCCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTACACTCAAGATCAGCAG 692
 DB 271 GTTCCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTACACTCAAGATCAGCAG 330
 QY 693 AGTGGAGGCTGAGGATCTGGGAGTTTATTCTGCTCTCAAAGTACACATGTTCCGCTACAC 752
 DB 331 AGTGGAGGCTGAGGATCTGGGAGTTTATTCTGCTCTCAAAGTACACATGTTCTCCGAC 390
 QY 753 GTTCCGAGGGGGGACCAAGCTGGAATAAAAA 783
 DB 391 GTTCCGAGGGGGGACCAAGCTGGAATAAAAA 421

RESULT 11

BQ933319
 LOCUS BQ933319
 DEFINITION AGENCOURT_8881916 NCI_CGAP_Co24 Mus musculus cDNA clone
 IMAGE:6476417 5', mRNA sequence.
 ACCESSION BQ933319
 VERSION BQ933319.1 GI:22348702
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 913)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: The Cepko Laboratory
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM14016 row: 1 column: 18
 High quality sequence start: 3
 High quality sequence stop: 525.
 Location/Qualifiers
 1..913
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:6476417"
 /clone_lib="NCI_CGAP_Co24"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.6 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

FEATURES

source

1..913
 /organism="Mus musculus"
 /strain="FVB/N"
 /db_xref="taxon:10090"
 /clone="IMAGE:6476417"
 /clone_lib="NCI_CGAP_Co24"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.6 kb. Constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT

ORIGIN

223 a 259 c 213 g 218 t

Query Match

35.4%; Score 293.6; DB 14; Length 913;

Best Local Similarity 91.5%; Pred. No. 1.3e-77;
Matches 311; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

Qy 444 CGGGATGTTGTGATGACCCCAACCCACTCTCCCTGCTGTGCTGTGAGATCAAGC 503
Db 105 CAGTATGTTTGTGATGACCCCAACCCACTCTCCCTGCTGTGCTGTGAGATCAAGC 164
Qy 504 CTCATCTCTTGCAGATCTAGTCAGAGCTTTTACACAGTAATGAATCACTATTACA 563
Db 165 CTCATTTCTTGCAGATCTAGTCAGAGTATGTACATAGTAATGGAATACCTTTTAGA 224
Qy 564 TTGTACTCTGAGAACCCAGCCAGCTCTCCAAAGCTCTCTGATCTACAAAGTTTCCAAACG 623
Db 225 ATGTTACCTGAGAAACCCAGCCAGCTCTCCAAAGCTCTCTGATCTACAAAGTTTCCAAACG 284
Qy 624 ATTTTCTGGGTCCTCCAGACAGGTTTCAGTGGCAGTGATCAGGACAGATTTTCACTCAA 683
Db 285 ATTTTCTGGGTCCTCCAGACAGGTTTCAGTGGCAGTGATCAGGACAGATTTTCACTCAA 344
Qy 684 GATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAAGTACACATGT 743
Db 345 GATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAAGTACACATGT 404
Qy 744 TCCGTACACTTTCGAGGGGGGACCAAGCTGGAATAAAA 783
Db 405 TCCGTGGAGCTTCGGTGGAGGACCAAGCTGGAATCAA 444

RESULT 12
AZ791472/c
LOCUS
DEFINITION 2M0041H23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M004H23 F, DNA sequence.
ACCESSION AZ791472
VERSION AZ791472.1 GI:12934393
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 509)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Ielam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausen,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0041 row: H column: 23
Seq primer: CGTTGTAACACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 509.
Location/Qualifiers
1..509
/organism="Mus musculus"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGC2M004H23"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
/notes="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (G14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT 124 a 127 c 128 g 130 t
ORIGIN

Query Match 33.8%; Score 280.8; DB 17; Length 509;
Best Local Similarity 97.8%; Pred. No. 8.7e-74;
Matches 285; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 69 GGTTCAACTGCAGCAGTCTGGGGCTGAGCTGGTGAGCCCTGGGGCTTCAGTGACGCTGTC 128
Db 327 GGTTCAACTGCAGCAGTCTGGGGCTGAGCTGGTGAGCCCTGGGGCTTCAGTGACGCTGTC 268
Qy 129 CTGCAAGGCTTCGGGGCTACACATTTACTGACTATGAATACACTGGGTGAGGCAGACACC 188
Db 267 CTGCAAGGCTTCGGGGCTACACATTTACTGACTATGAATACACTGGGTGAGGCAGACACC 208
Qy 189 TGTGCATGGCTGGAATGGATTTGAGAGCTATTGATCTCGAACTGGTGGTACTGCTTCAA 248
Db 207 TGTGCATGGCTGGAATGGATTTGAGAGCTATTGATCTCGAACTGGTGGTACTGCTTCAA 148
Qy 249 TCAGAAGTTCAAGGACAAGCCATAGTACTGTAGACAAATCTCCAGCAGACGCTACAT 308
Db 147 TCAGAAGTTCAAGGACAAGCCATAGTACTGTAGACAAATCTCCAGCAGACGCTACAT 88
Qy 309 GGAGCTCCGAGCCTGACATCTGAAAGACTCTGCGGCTATTACTATATACAAGA 360
Db 87 GGAGCTCCGAGCCTGACATCTGAGGACTCTGCGGCTATTACTGTACAAGA 36

RESULT 13
BF135785
LOCUS
DEFINITION 601782072F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4010344 5', mRNA linear EST 24-OCT-2000
ACCESSION BF135785
VERSION BF135785.1 GI:10974825
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 898)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9247 row: 0 column: 17
High quality sequence stop: 4
High quality sequence start: 520.
Location/Qualifiers

REFERENCE 1
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

FEATURES

FEATURES
source

Location/Qualifiers

1. .884
/organism="Mus musculus"
/strain="FVB/N"
/db xref="taxon:10090"
/clone="IMAGE:4985875"
/clone_lib="NCI_CGAP_Co24"
/lab_host="DH10B (TI phage-resistant)"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
BASE COUNT 221 a 269 c 182 g 212 t
ORIGIN

Query Match 33.5%; Score 277.8; DB 13; Length 884;
Best Local Similarity 90.3%; Pred. No. 8.2e-73;
Matches 308; Conservative 0; Mismatches 32; Indels 1; Gaps 1;
QY 443 CCGGGGATGTTGATGACCCCAACCCACTCTCCCTGCGCTGTCAGTCTTGGAGATCAAG 502
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
18 CCACTGATGTTTGTGACCCCAAACTCCACTCTCCCTGCGCTGTCAGTCTTGGACTTCAAG 77
QY 503 CCTCATCTCTTGCGAGATCTAGTCAGAGCCCTTTACACAGTAATGGAATCACCTATTAC 562
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
78 CCTCATCTCTTGCGAGATCTAGTCAGAGCATTTTAAATAGTGATGGAAACACCTATTAG 137
QY 563 ATGGTACCTGCGAAGCCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAAAC 622
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
138 AATGTTCTCTGCA-AAACCAGGCCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAAAGC 196
QY 623 GATTTCTGGGGTCCCAGACAGGTTTCAGTGGCAGTGGATCAGGGACAGATTTCACACTCA 682
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
197 GATTTCTGGGGTCCCAGACAGGTTTCAGTGGCAGTGGATCAGGAACAGATTTCACACTCA 256
QY 683 AGATCAGCAGATGGAGGCTGAGGATCTGGAGTTTATTTCTGCTCTCAAGTACACATG 742
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
257 AGATCAGCAGATGGAGGCTGAGGATCTGGAGTTTATTTACTGCTTTTCAAGGTTACATG 316
QY 743 TTCCGTACACGTTCCGAGGGGGGCAAGCTGGAAATAAAA 783
Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
317 TTCCATTACGTTCCGGCTCGGGGACAAAGTTGGAAAGTAGAA 357

Search completed: May 17, 2003, 05:35:20
Job time : 1138 secs

Query Match	61.5%	Score 510.8	DB 10	Length 879
Best Local Similarity	80.1%	Prod. No. 4.8e-154		
Matches 634	Conservative	0	Mismatches 137	Indels 21
Gaps				
46	GCGGGCCATTCTGCCTTTTCGGCGGTTCAACTGCAGCAGTCTGGGGCTGCAGCTGGTGAGG	105		
46	GCGGGCCAGCGGCCATGCCCAGGTCCAACTGCAGCAGTCTGGACCTGCAGCTGGGAGAAG	105		
106	CTGGGGCTTCAGTCAGCGTCTCTGCAAGGCTTCGGGCTACACATTTACTGACTATGAA	165		
106	CTGGCGCTTCAGTCAGATATCCTGCAAGGCTTCGGTTACTCATTCACTGACTACAAC	165		
166	ATACACTGGGTGAGGCAGACCTGTGCATGCGCTTGGAAATGAAATGGACCTATTGATCT	225		
166	ATGAACCTGGTGAAGCAGAGCAATGGAAGAGCCTTTGAGTGGATTGGAAATATTGATCT	225		
226	GAACCTGGTGTTACTGCCTTACAATCAGAAGTTCAAGGCAAGGCCCATGACTGACTAGAC	285		

Db 226 TACTATGTTGGTACTAGTTAAATCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGAC 285
 Qy 286 AAATCTCTCAGCAGCAGCTACATGGAGCTCCGAGCCTGACATCTGAAGACTCTGCGCTC 345
 Db 286 AAATCTCTCAGCAGCAGCTACATGGAGCTCCGAGCCTGACATCTGAAGACTCTGCGCTC 345
 Qy 346 TATTACTATACAGATGGTTTGGAGACTGGGGCCAAAGGACTCTGGTCACTGTCTCTGCA 405
 Db 346 TATTCTGTGCAAGATGGGACTATAGTTACGACGACGGGAGGCTTACTATGTTATGGAC 405
 Qy 406 GAGGGTAAATCTCAGGATCTGGCTCGAATCAAACCCGG-----GGATGTTGTG 456
 Db 406 TTCTGGGGCCAAAGGACCCAGCTGACCGCTCTCTCAAGCGGTGGCGGATCGGCACATTGAG 465
 Qy 457 ATGACCCCAAAACCCACTCTCCCTGCGCTGTGAGTCTGAGTCAAGCTTCAAGCTTCTTGC 516
 Db 466 CTCACTAGTCTCACTCTCCCTGCGCTGTGAGTCTGAGTCAAGCTTCAAGCTTCTTGC 525
 Qy 517 AGATCTAGTCAAGCTCTTACAGTAAATGGAATCACTTATTTACATTTGTTGCTGCGAG 576
 Db 526 AGATCTAGTCAAGCTCTTGAACAGTAAATGGAATCACTTATTTACATTTGTTGCTGCGAG 585
 Qy 577 AAGCCAGGCGAGTCTCAAAGCTCTGATCTCAAAAGTTTCCAAAGCTTCTTGGGCTC 636
 Db 586 AAGCCAGGCGAGTCTCAAAGCTCTGATCTCAAAAGTTTCCAAAGCTTCTTGGGCTC 645
 Qy 637 CCAGACAGGTTTCAAGTGGAGTCAAGGACAGATTTTCACTCAAGATCAGCAGAGTG 696
 Db 646 CCAGACAGGTTTCAAGTGGAGTCAAGGACAGATTTTCACTCAAGATCAGCAGAGTG 705
 Qy 697 GAGGCTGAGGATCTGGAGTTTATTTCTGCTCTCAAAGTACACATGTTCCGTACAGCTTC 756
 Db 706 GAGGCTGAGGATCTGGAGTTTATTTCTGCTCTCAAAGTACACATGTTCCGTGAGCTTC 765
 Qy 757 GGAGGGGGACCAAGCTGGAATATA-----AGAGAAAACTCATCTCAGAA 804
 Db 766 GTGGAGGACCAAGCTGGAATATAACCGGCGCGCCGACAGAAAACTCATCTCAGAA 825
 Qy 805 GAGGATCTGAAT 816
 Db 826 GAGGATCTGAAT 837

RESULT 2
 US-09-203-958-2
 ; Sequence 2, Application US/09203958
 ; Publication No. US20030039641A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tibor Keller, et al.
 ; TITLE OF INVENTION: CELLS EXPRESSING ANTI-Fe RECEPTOR BINDING COMPONENTS
 ; FILE REFERENCE: MXI-099
 ; CURRENT APPLICATION NUMBER: US/09/203,958
 ; CURRENT FILING DATE: 1998-12-02
 ; EARLIER APPLICATION NUMBER: 60/067,232
 ; EARLIER FILING DATE: 1997-12-02
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 1135
 ; TYPE: DNA
 ; ORGANISM: synthetic construct
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (74)..(1132)
 US-09-203-958-2

Query Match 50.5%; Score 419.4; DB 9; Length 1135;
 Best Local Similarity 72.0%; Pred. No. 1.4e-124;
 Matches 588; Conservative 0; Mismatches 196; Indels 33; Gaps 2;
 Qy 43 GCGGCGGCGGATCTGCTTTGGCGGCTTCAAGCTGAGGCTGCGGCTGAGCTGGTG 102
 Db 161 GCTGGGCGGCGGCGGCGGCTGAGATCTGAGTCAAGCTGAGGCTGAGCTGAGCTGGTG 220

Qy 103 AGGCTGGGGCTTCAGTGACGCTGTCTGCAAGGCTTCGGGCTACACATTTTACTGACTAT 162
 Db 221 AAGCTTGGGGCTTCAGTGAAGATATCTGCAAGGCTTCGGTATTCATTTACTGACTAC 280
 Qy 163 GAAATACACTGGGTGAGGACAGACACCTGTGCAATGAGGCTTGAATGGAATGGAATTTGAT 222
 Db 281 ATCATATTTGGGTGAAGCAGAGCCATGAAAGAGCTTGTAGTGACTGGAATAATAAT 340
 Qy 223 CCTGAAATCTGGTGTACTGCTTACATCAGAGTTTCAAGGCAAGGCCATAGTACTGTA 282
 Db 341 CCTTACTATGGTAGTACTAGTACCAATCTGAAGTTTCAAGGGCAAGGCCACATTTGACTGTA 400
 Qy 283 GACAAATCTCTCAGCAGACGCTTACATGAGCTTCCGAGCTTCCAGCTTCAAGCTTCTGCGC 342
 Db 401 GACAAATCTTCCAGCAGACGCTTACATGAGCTTCAAGCTTCAAGCTTCTGAGGACTCTGCA 460
 Qy 343 GTCTATTACTATACAAGATG-----GTTTGGAGGAC 372
 Db 461 GTCTATTACTGTGAAGAGGAGTTTATTACTACGGTAGTAGCTACGAGGCGTTTCTCTTAC 520
 Qy 373 TGGGGCCAGGAGCTCTGCTCACTGCTCTGCGAGAGGT---AAATCTCTCAGGACTCTGCG 429
 Db 521 TGGGGCCAGGAGCTCTGCTCACTGCTCTGCGAGAGGTGCGGCTCCGAGGAGGCTGCG 580
 Qy 430 TCCGAATCCAAACCGGGATGTTGTGATGACCCCAACCCACTCTCCCTGCTCTGCTCACT 489
 Db 581 ACCGAGGGGGCGGATCCGATGTTGTGATGACCCAGACTCCACTCACTTTGTGCTGATTACC 640
 Qy 490 CTGAGATCAAGCTTCCATCTTTGCGAGATCTAGTCAAGGCTTTTACACAGTAAATGGA 549
 Db 641 ATTGACAAACAGCTTCCATCTCTTGAAGTCAAGTCAAGGCTTCTAGATAGTATGGA 700
 Qy 550 ATCACTATTTTACATGTTGCTGAGAGGCTGAGGCTTCCGAGGCTTCCGAGCTCTGATCTAC 609
 Db 701 AAGACATATTTGAATTTGTTTACAGAGGCGGAGGCTTCCGAGGCTTCCGAGGCTTCTAT 760
 Qy 610 AAAGTTTCAACCGGATTTTCTGGGGTCCAGACAGCTTCAAGTGGAGTGGATCAGGAGCA 669
 Db 761 CTGGTGTCTAACTGGACTCTGGAGTCTTCAAGCTTCAAGTGGAGTGGATCAGGAGCA 820
 Qy 670 GATTTCACTCAAGATCAGCAGAGTGGAGCTGAGGATCTGGGAGTTTATTTCTGCTCT 729
 Db 821 GATTTCACTCAAGATCAGCAGAGTGGAGCTGAGGATTTGGGAATTTATTTTCTGCTGG 880
 Qy 730 CAAAGTACACATGTTCCGTACACGTTCCGAGGGGGGAGCCAGCTGGAATAAAGAGNA 789
 Db 881 CAAGGTGACATTTTCTCAGACGTTCCGAGGCGGAGGCTTCCGAGGCTTCCGAGGCTTCTAT 940
 Qy 790 AAATCTCATCTCAGAAAGAGGATCTGAATTTAGTAAGCGG 826
 Db 941 CTGAGGTCGAGCAACAAAACATCATCTCAGAGAGG 977

RESULT 3
 US-09-968-851-46
 ; Sequence 46, Application US/09968851
 ; Publication No. US20020193561A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CONSEILLER, EMMANUEL
 ; BRACCO, LAURENT
 ; TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
 ; USES THEREOF
 ; NUMBER OF SEQUENCES: 59
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
 ; DUNNER, LLP
 ; STREET: 1300 I Street, NW
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-3315
 ; COMPUTER READABLE FORM:

[illegible]

RESULT 4
US-09-968-851-37
; Sequence 37, Application US/09968851
; Publication No. US2002193561A1
; GENERAL INFORMATION:
; APPLICANT: CONSEILLER, EMMANUEL
; BRACCO, LAURENT
; TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
; USES THEREOF
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNIGAN, HENDERSON, FARABOW, GARRETT &
; DUNNER, LLP
; STREET: 1300 I Street, NW
; CITY: Washington

Query Match	48.8%	Score 405.2;	DB 9;	Length 1611;
Best Local Similarity	74.1%	Pred. No. 5.9e-120;		
Matches 544:	Conservative	0;	Mismatches 178;	Indels 12;
				Gaps

62	TTGGGGCGGTTCAACTGCAGAGCTCTGGGCTGAGCTGGTGAGGCCTTGGGCTTCAGTGA	121	QY
2	TGGCCAGGTGCAGTCGAGAGTCAGGGCAGAGCTTGTGGGTGAGGGCCCTCAGTCA	61	Db
122	CGCTGTCTCGAAGGCTTCGGGCTACACATTTACTGACTATGAAATACACTGGGTGAGC	181	QY
62	AGTTGCTCGCAGCTTCTGGCTTCAACATTAAGACTACTATATGCACTGGGTGAAGC	121	Db
182	AGACACCTGTGCATGGCTCGGAATGGATTGAGACTATTGATCTGAAACTGGTGTTACTG	241	QY
122	AGAGGCTGAACAGGGCTCGAGTGGATTGGATTGATCTTGAGATGGTGATCTG	181	Db
242	CCTACAAATCAGAAGTTCAAGGACAAGGCCATAGTGACTGTAGACAAATCCTCCAGCACAG	301	QY
182	AATATGCCCCGAAGTTCAGGGCAAGGCCACTATGACTGCAGACACATCCTCCAATACAG	241	Db
302	CCTACATGGAGCTCCGAGGCTGACATCTGAAGACTCTGCCGTCTATTACTATACAAGAT	361	QY
242	CCTACCTGCAGCTCAGCAGGCTGGCATCTGAGGACACTGCCGTCTATTATTGTAATTTT	301	Db
362	-----GGTTTGAGGACTGGGCCAAGGACTCTGGTCACTGTCTCTGCAGAGGTTA	412	QY
302	ACGGGAGTCTTTGGACTCTGGGGCCAAGGGACACGGTCAACCGTCTCCTCAGGTGGAG	361	Db
413	AATCCTCA---GGATCTGGCTCCGAATCCAAACCGGGGATGTTGTGATGACCCCAAAC	469	QY
362	GCGGTTCAGCGGAGTGGCTCTGGCGGTGGCGATCGGATGTTTGTAGACCCAAACTC	421	Db
470	CACCTCCCTCCCTGTGAGTCTTGGAGATCAAGCCTCCATCTCTTGACAGATCTAGTCAGA	529	QY
422	CACCTCACTTTGTCCGTTACCATTTGGACAACAGCGCTCCATCTCTTGCAAGTCAAGTCAGA	481	Db
530	GCCTTTTACACAGTAATGGAATCACCTATTTCATTTGGTACCTGCAAGAGCCAGGCCAGT	589	QY
482	GCCTCTTGGATAGTGTGGAAGACATATTTGAATTTGGTTGTGTACAGAGCCAGGCCAGT	541	Db
590	CTCCAAGCTCCTGATCTACAAGTTTCCAACCGATTTTCTGGGTCCCAAGCAGGTTC	649	QY
542	CTCCAAGCGCCTAATCTATCTGGTGTCTAACTGGGACTCTGGAGTCCCTGCACAGGTTC	601	Db
650	GTGCGAGTGGATCAGGGACAGATTTTCACACTCAAGATCAGCAGATGGAGGCTGAGGATC	709	QY
602	CTGGCAGTGGATCAGGGACAGATTTTCACCTGAAATTCACAGATGGAGCTGAGGATTT	661	Db
710	TGGGAGTTTATTTCTGCTCTCAAAGTACACATGTTCCGTACAGTTTCGGAGGGGGACCA	769	QY
662	TGGGAGTTTATTTGCTGCAAGGTACACATTTCCGCTCACTCGTTCGGTCTGGGACCA	721	Db
770	AGCTGGAAATAAAA	783	QY
722	AGCTGGAGCTGAAA	735	Db

[illegible]

```

; TITLE OF INVENTION: INDOUCTION OF I CELL TOLERANCE WITH
;
; TITLE OF INVENTION: CD40/B7 antagonists
;
; FILE REFERENCE: 99-1
;
; CURRENT APPLICATION NUMBER: US/09/978,752
;
; CURRENT FILING DATE: 2001-10-15
;
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/235,073
;
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-21
;
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/NL97/00438
;
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-23
;
; NUMBER OF SEQ ID NOS: 22
;
; SOFTWARE: FastSEQ for Windows Version 3.0
;
; SEQ ID NO 7
;

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; PRIOR FILING DATE: 2000-07-03
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 4661
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-897-006-10

Query Match 42.3%; Score 351.4; DB 10; Length 4661;
Best Local Similarity 70.7%; Pred. No. 1.9e-102; Indels 12; Gaps 3;
Matches 514; Conservative 0; Mismatches 201; Indels 12; Gaps 3;

Qy 69 GTTCAACTGCAGCAGTCTGGGGCTGAGCTGTGAGGCTGGGGCTTCAGTGAGCGCTGTC 128
Db 2157 GGTTCAGTTGCAGCAGTCTGAGCGTGAAGTGTGTAAGCTGGGGCTTCAGTGAAGATTTC 2216
Qy 129 CTGCAAGGCTTGGGCTACATTTACTGACTATGAATATACACTGGGTGAGGCAGACACC 188
Db 2217 CTGCAAGGCTTCTGGCTACACCTTCACTGACCATGCAATTCAGTGGTGAACAGAACCC 2276
Qy 189 TGTGCATGGCTGGATGGATGGAGCTATTGATCCTGAACTGGTGTACTGCTACAA 248
Db 2277 TGAACAGGGCTGGGAATGGATGGATATTTTCTCCCGAAATGATGATTTAAATCAA 2336
Qy 249 TCAGAAGTTCAAGACAAGGCGCATAGTCACTGTAGACAAATCCTCCAGCAGACCTACAT 308
Db 2337 TGAGAGTTCAAGGCGAAGCCACACTCACTGCAGACAAATCCTCCAGCAGTGCCTAGT 2396
Qy 309 GGAGTCCGAGCCTGACATCTGAAGATCTTGCCTGTCTATTACTATACAAGT-----G 362
Db 2397 GCAGCTCAACAGCCTGACATCTGAGGATTTCTGAGTGTATTCTGTACAAGATCCCTGAA 2456
Qy 363 GTTTCAGGACTGGGCGCAGGAGCTCTGGTCACTGTCTCTGAGAGGTTAA---TCTC 419
Db 2457 TATGGCTTACTGGGGTCAAGGAACCTCAGTCACTGCTCTCTCAGAGGCGGAGGCGG 2516
Qy 420 AGGATCTGGCTCCGAATCCAAACCGGGGATGTTGTGATGACCCCAACCCACTCTCCCT 479
Db 2517 AGGCGTGGCTCGGAGGCGGAGGCTCGGACATTTGTGATGTCACAGTCTCCATCTCCCT 2576
Qy 480 GCCTGTAGTCTTGAGATCAAGCCTCCATCTCTTTGAGATCTAGTCAGAGCCTTTTACA 539
Db 2577 ACCTGTGAGTTGGCGAAGAGTTACTTTGAGCTGCAAGTCCAGTCAAGAGCCTTTTATA 2636
Qy 540 CA---GTAATGGAATCACTATTATTTACATTTGGTACCTGAGAGCCAGGCCAGTCTCCAA 596
Db 2637 TAGTGGTAATCAAAAGAACTACTTGGCTGGTACCAGCAGAAACCGAGGCGAGTCTCTAA 2696
Qy 597 GCTCTGATCTACAAAGTTTCCAAACCGGATTTTCTGGGCTCCAGACAGGTTCAAGTGGCAG 656
Db 2697 ACTGCTGATTTACTGGGATCCGCTAGGGAATCTGGGTCTCCATGCTTCAAGGCGAG 2756
Qy 657 TGGATCAGGACAGATTTTCACTCAAGATCAGCAGAGTGGAGGCTAGGATCTGGGAGT 716
Db 2757 TGGATCTGGGACAGATTTTCACTCTCTCCATCAGCAGTGTGAAGACTGAAGACCTTGGCAGT 2816
Qy 717 TTATTTCTGCTCTCAAGATACATGTTCCGTACACGTTTCGAGGGGGGACCAAGCTGGA 776
Db 2817 TTATTTCTGTCAGCAGTATTATAGCTATCCCTCAGTTCGGTCTGGGACCAAGCTGGT 2876
Qy 777 AATAAAA 783
Db 2877 GCTGAAA 2883

RESULT 7
US-09-924-099-20
; Sequence 20; Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:

; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 20
; LENGTH: 729
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial DNA to code for the amino acid sequence of
; OTHER INFORMATION: SEQ
; OTHER INFORMATION: ID NO:10
US-09-924-099-20

Query Match 40.2%; Score 334; DB 10; Length 729;
Best Local Similarity 68.3%; Pred. No. 3.6e-97;
Matches 504; Conservative 0; Mismatches 210; Indels 24; Gaps 2;

Qy 67 GCGGTTCAACTGCAGCAGTCTGGGGCTGAGCTGGTGGAGCCTGGGGCTTCAGTGACGCTG 126
Db 1 GAGATCCAGCTGCAGCAGTCTGGACCTGAGCTGGTGAAGCCTGGGGCTTCAGTGAAGTTC 60
Qy 127 TCCTGCAAGGCTTCGGGCTACACATTTTACTGACTATGAAATATACACTGGGTGAGGCAGACA 186
Db 61 TCCTGTAAGGCTTCGGTACTCACTCACTGACTACTTCAITTTACTGGTGAACGAGCAGC 120
Qy 187 CTTGTGCATGCCCTGGAAATGGATTGGAGCTATTGATCCTGAAACTGGTGGTACTGCCCTAC 246
Db 121 CATGAAAGAGCCTTGAAGTGGATTTGAGATATTGATCCTTATATGTTGATAGTATTAC 180
Qy 247 AATCAGAAGTTCAAGGACAAGGCCATAGTCACTGACAGCAAAATCCTCAGCAGCAGCTAC 306
Db 181 AACAGAAGTTTCAAGGACAAGGCCATAGTCACTGTTGACCAGTCTCCACACAGCCTTC 240
Qy 307 ATGAGAGTCTGGCAGCCTGACATCTGAAAGACTCTGCCCTCTATTACTATACAAGATGGTT 366
Db 241 ATGCATCTCAACAGCCTGACATCTGAGGACTCTGCACTCTATTCTGTGCAAGAGGCTTA 300
Qy 367 GAGGAGTGGGGCCAAAGGAGTCTTGGTCACTGTCTCTGCA-----GAGGGTAAATCC 417
Db 301 CGGTTCTGGGGCCAAAGGAGTCTTGGTCACTGTCTCTGAGGTGGAGGTGGAGGCGGATCC 360
Qy 418 TCAGGATCTGGCTCCGAATCCAAACCCGGGATGTTGTGATGACCCCAAAACCCACTCTCC 477
Db 361 GGGGAGGTGGCTCTGGGGTGGCGGATTCGGACATCCAGATGACCCAGTCTCCATCTCC 420
Qy 478 CTGCTGTGAGTCTTGAGAGATCAAGCCTCCATCTCTTGCAGATCTAGTCAGAGCCTTTTA 537
Db 421 TTATCTGCTCTCTGGGAGAAAGAGTCACTCACTGTCTGGGCAAGTCAGGACATT--- 477
Qy 538 CACAGTAATGAATCACTATTATACATTTGATGCTGAGAGCCAGGCCAGTCTCCAAAG 597
Db 478 -----GGTAGTAAATTTATCTGCTTCAACAGGAACCCAGATGGAACCTTTTAA 525
Qy 598 CTCTGATCTACAAAGTTTCCAAACCGATTTTCTGGGCTCCAGACAGGTTCAAGTGGCAGT 657
Db 526 CGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTGTCCCAAGAGGTTCAAGTGGCAGT 585
Qy 658 GGATCAGGAGCAGATTTTCACTCAAGATCAGCAGAGTGGAGGCTGAGGATCTGGGAGTT 717
Db 586 AGGTCTGGGTGAGATTTCTCTCACCATCAGCAGCCTTGAAGATTTTGTAGAC 645

QY 718 TATTCTGCTCTCAAGTACACATGTTCCGTACACGTTTCGGAGGGGGGACCAAGCTGGAA 777
| | | | |
Db 646 TATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGGGGGACCAAGCTGGCA 705
| | | | |
QY 778 ATAAAGAGAAAAAATC 795
| | | | |
Db 706 ATAAACATCAACCATCAC 723
| | | | |

RESULT 8

US-09-924-099-19
; Sequence 19, Application US/09924099
; Patent No. US20020128450A1
; GENERAL INFORMATION:
; APPLICANT: NISHIDA, Yoshihiro
; APPLICANT: OKURA, Takanori
; APPLICANT: TANIMOTO, Tadao
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: PEPTIDE
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/924,099
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 19
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial DNA to code for the amino acid sequence of
; OTHER INFORMATION: SEQ
; OTHER INFORMATION: ID NO: 9
US-09-924-099-19

Query Match 40.1%; Score 333.2; DB 10; Length 711;
Best Local Similarity 68.7%; Pred. No. 6.4e-97;
Matches 499; Conservative 0; Mismatches 203; Indels 24; Gaps 2;
2Y 67 GCAGTCACTGACGAGCTCTGGGCTGAGCTGGTGGGCTTGGGCTTCAGTGGAGCTG 126
| | | | |
2b 1 GAGATCCAGCTGACGAGCTGAGACCTGAGCTGGTGAAGCTTGGGCTTCAGTGAAGTTC 60
| | | | |
2Y 127 TCTGCAAGCTTGGGCTACACATTTACTGACTATGAATACATCACTGGGTGAGGACAGCA 186
| | | | |
2b 61 TCTGTGAAGCTTCTGGTTACTCACTGACTTCTTCACTTCTGAGTGAAGCAGAGC 120
| | | | |
2Y 187 CTTGTGATGCGCTGGAATGATGAGCTATTGATCTTGAAGCTTGAAGCTTGAAGCTTGA 246
| | | | |
2b 121 CATGGAAGAGCTTGGTGGATGGAGATATTGATCTTATATGATGATAGTATTAC 180
| | | | |
2Y 247 AATCAGAAGTTCAAGGACAGGCTAGTACTGATGACATCAAGAAATCTCCAGCAGAGCTAC 306
| | | | |
2b 181 AACCAGAAGTTCAAGGACAGGACACATTCAGTGTGACAGCTCTCCACACAGCCTTC 240
| | | | |
2Y 307 ATGAGCTCGGAGCTGACATCTGAAGACTCTGCGTCTATTACTATACAAAGATGTTT 366
| | | | |
2b 241 ATGATCTCAACAGCTGACATCTGAGGACTCTGCAGTCTATTCTGTGCAAGAGGCTTA 300
| | | | |
2Y 367 GAGGACTTGGGCAAGGAGCTCTGGTCACTGTCTCTGCA-----GAGGTAATATCC 417
| | | | |
2b 301 CGTTTCTGGGGCAAGGAGCTCTGGTCACTGTCTCTGAGAGTGGAGGCGGATCC 360
| | | | |
2Y 418 TCAGGATCTGGCTCCGAATCCAAACCCGGGATGTTGTGATGACCCCAACCCACTCTCC 477
| | | | |
2b 361 GCGGAGGTGGCTCTGGCGTGGCGATCGACATCGACATGACCATGACCCAGTCTCCATCTCC 420
| | | | |
2Y 478 CTGCTGTGAGTCTTGGAGATCAAGCCTCCATCTCTTTCAGATCTTAGTCAAGAGCCTTTTA 537
| | | | |

Db 421 TTATCTGCCCTCTCTGGAGAAAGAGTCAGTCTCACTTGTTCGGCAAGTCAGGACATTTG-- 478
| | | | |
QY 538 CACAGTAATGGAATCACCTTATTACATTGGTACCTGCGAAGCCAGGCCAGTCTCCAAAG 597
| | | | |
Db 479 -----GTAGTAATATTACTGGCTTCAACAGGAACAGATGGAACATTTTAA 525
| | | | |
QY 598 CTCCTGATCTACAAAGTTTCCAAACCGATTTCTGGGGTCCACAGAGTTTCAGTGGCAGT 657
| | | | |
Db 526 CGCCTGATCTACGCCACATCCAGTTTAGATTCTGGTCTCCCAAGAGGTTTCAGTGGCAGT 585
| | | | |
QY 658 GGATCAGGACAGATTTACACTCAAGATCAGCAGATCGGAGCTGAGGATCTGGAGTT 717
| | | | |
Db 586 AGGTCTGGGTGAGATTATTCTCTCACCATCAGCAGCTTGAAGTCTGAAGATTTTGTAGAC 645
| | | | |
QY 718 TATTCTGCTCTCAAAAGTACACATGTTCCGTACAGCTTCGGAGGGGGACCAAGCTGGAA 777
| | | | |
Db 646 TATTACTGTCTACAATATGCTAGTTCTCCGTACACGTTTCGGAGGGGGGACCAAGCTGGCA 705
| | | | |
QY 778 ATAAAA 783
| | | | |
Db 706 ATAAAA 711
| | | | |

RESULT 9

US-10-060-585-6
; Sequence 6, Application US/10060585
; Publication No. US20030083290A1
; GENERAL INFORMATION:
; APPLICANT: Kingsman, Alan J.
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Carroll, Miles W.
; APPLICANT: Ellard, Fiona M.
; APPLICANT: Kingsman, Susan M.
; APPLICANT: Myers, Kevin A.
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: DYOU23.00ICPI
; CURRENT APPLICATION NUMBER: US/10/060,585
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 09/445375
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: GB 9711579.4
; PRIOR FILING DATE: 1997-06-04
; PRIOR APPLICATION NUMBER: GB 9713150.2
; PRIOR FILING DATE: 1997-06-20
; PRIOR APPLICATION NUMBER: GB 9714230.1
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/GB99/03859
; PRIOR FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 2090
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 514 ScFv - human IgE fusion
US-10-060-585-6

Query Match 38.7%; Score 321; DB 9; Length 2090;
Best Local Similarity 67.1%; Pred. No. 8.3e-93;
Matches 519; Conservative 0; Mismatches 215; Indels 39; Gaps 3;
QY 35 TTTTCGGCGCGCGGCGCATTTCTGCTTTGCGCGGTTCAACTGCAGCAGTCTGGGCTG 94
| | | | |
Db 37 TCTTGTAGAACAACTACAGGTGTCCACTCCGAGGTCCAGCTGCAGCAGTCTGGACCTG 96
| | | | |
QY 95 AGCTGGTGAAGCTTGGGCTTCAGTGAGCTCTCTGCAAGGCTTCGGGCTACACATTTA 154
| | | | |
Db 97 ACCTGGTGAAGCTTGGGCTTCAGTGAAGATATCTGCNAGGCTTCTGGTACTCATTC 156
| | | | |
QY 155 CTGACTATGAATAACATCGGTGAGGACAGACCTGTGATGCGCTGGAATGGATTGGAG 214
| | | | |

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157 CTGGCTACTACATGCTGGTGAAGCAGAGCCATGAAGAGCCCTTGGTGGATTGGAC 216
215 CTATTGATCTGAACTGGTGGTACTGCTACATCAGAAAGTTCAAGCAAGGCCATAG 274
217 GTATTATCTTACAAATGGTGGTACTCTTACACCAAGAAATCAAGGACAGGCCATAT 276
275 TGACTGTAGACAAATCTCCAGCAGACGCTTACATGGAGTCCGAGCCTGACATCTGAAG 334
277 TAACTGTAGACAAAGTATCACCACAGCCTACATGGAGTCCGAGCCTGACATCTGAGG 336
335 ACTCTGCGGTCTATTACTATACAGAT-----GGTTTCAGGACT 373
337 ACTCTGCGGTCTATTACTGTGAAGATCTACTATGATGAACTATGTTATGGACTACT 396
374 GGGCCCAAGGACTCTGGTCACTGCTCTGAGAGGGTAAATCTCAGGATCTGGCTCCG 433
397 GGGGTCAAGTAACTTCACTGATCAGTCCCTCTTTCAGGTGGTGGAGCGGTGGCGGCA 456
434 AATCCAAACCCGG---GGATGTTGTGATGATGACCCCAACCCACTCTCCCTGCTGTGATC 490
457 CTGCGCGGCGGATAGTATTGATGATGATGATGATGATGATGATGATGATGATGATG 516
491 TTGGAGATCAAGCCTCCTCTCTTGCAGATCTAGTCAAGCCTTTTACAGTAATGGAA 550
517 CAGGAGACAGGGTTACCATACCTGCAAGGCCAGTCAGAG-----TGTA 561
551 TCACCTATTTACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 610
562 GTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 621
611 AAGTTTCCAAACCCGATTTCTGGGTGATGATGATGATGATGATGATGATGATGATGAT 670
622 ATACATCCAGTCGCTAGCTGAGTCCCTGATGATGATGATGATGATGATGATGATGATG 681
671 ATTTCACTCAAGATCAGAGATGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 730
682 ATTTCACTTTCCACATCAGCACTTTGAGGCTGAAGACCTGGCAGTTTATTTCTGTG 741
731 AAGTACACATGTTCCGTTACACGTTGAGGAGGGGAGCAAGCTGGAAATAAAA 783
742 AAGATTATATTTCTCTCCGAGCTTGGTGGAGGACCAAGCTGGAAATAAAA 794

RESULT 10
US-09-753-436-44
; Sequence 44, Application US/09753436
; Patent No. US20010029293A1
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Vazeux, Rosemay
; TITLE OF INVENTION: ICAM-Related Materials and Methods
; NUMBER OF SEQUENCES: 120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09753.436
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/382,289
; FILING DATE:
; APPLICATION NUMBER: US 08/487,113
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; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,754
; FILING DATE: 05-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/102,852
; FILING DATE: 05-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/009,266
; FILING DATE: 22-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/894,061
; FILING DATE: 05-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/889,724
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/827,689
; FILING DATE: 27-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Joseph A., Jr.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 33282
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 384 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-753-436-44

Query Match 38.6%; Score 320.4; DB 10; Length 384;
Best Local Similarity 96.7%; Pred. No. 6.5e-93;
Matches 327; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 446 GGGATGTTGTGATGACCCCAACCCACTCTCCCTGCTGCTGTCAGTCTTGGAGATCAAGCCT 505
DB 47 GTGACGCTGTGATGACCCCAACCTCCACTCTCCCTGCTGCTGTCAGTCTTGGAGATCAAGCCT 106

QY 506 CCATCTCTTGCAGATCTAGTCAGAGCCTTTTACACAGTAATGGAATCACCTATTTCATT 565
DB 107 CCATCTCTTGCAGATCTAGTCAGAGCCTTTGTACACAGTAATGGAATCACCTATTTCATT 166

QY 566 GTTACCTGCAGAAAGCCAGGCCAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCGAT 625
DB 167 GGTACCTGCAGAAAGCCAGGCCAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCGAT 226

QY 626 TTTCTGGGTCCAGACAGCTTCAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 685
DB 227 TTTCTGGGTCCAGACAGCTTCAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGT 286

QY 686 TCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAAAGTACATGTTTC 745
DB 287 TCAGCAGAGTGGAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAAAGTACATGTTTC 346

QY 746 CGTACACGTTTCGAGGGGGGACCAAGCTGGAAATAAAA 783
DB 347 CGTACACGTTTCGAGGGGGGACCAAGCTGGAAATAAAA 384

RESULT 11
US-09-518-737-3
; Sequence 3, Application US/09518737
; Publication No. US20030008321A1
; GENERAL INFORMATION:
; APPLICANT: FUKUI, YASUHIKA
; APPLICANT: NAGATA, SATOSHI
; APPLICANT: SHIRAI, RYUICHI
```



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QY 245 ACAATCAGAAAGTTCAAGGCAAGGCCATAGTACTGTAGACAAATCTCCAGCACAGCCT 304
DB 917 ACACACCAAAATTCAGGACACAGGCCATTAATCTGTAGACAAAGTCAATCCACACAGCCT 976
QY 305 ACATGGAGCTCCGAGGCTGACATCTGAAGACTCTGGCGTCTATTACTATACAAGAT--- 361
DB 977 ACATGGAGCTCCGAGGCTGACATCTGAGGACTCTGGCGTCTATTACTGTGCAAGATCTA 1036
QY 362 -----GGTTTCAGGACTGGGCGCAAGGACTCTGGTCACTGTCTCTG 403
DB 1037 CTATGATTAGAACTATGTTATGGACTACTGGGTCAAGTAACCTCAGTCACCGTCTCCT 1096
QY 404 CAGAGGTAATCTCAGGACTCTGGCTCCGAATCCAAACCCCGGG---ATGTTGTGATGA 460
DB 1097 CAGGTGTGTGGGAGCGGTGTGGCGCACTGGCGCGCGGATCTAGTATTGTGATGA 1156
QY 461 CCCCAACCCACTCTCCTGCTGTAGTCTTGGAGATCAAGCCTCCTATCTTTCGAGAT 520
DB 1157 CCCAGACTCCCACTCTCCTGCTGTTTTCAGCAGGAGACAGGGTTTACCATAACCTGCAAGG 1216
QY 521 CTAGTCAGAGCCTTTTACACAGTAATGGAATCACTATTATACATTTGTGTACCTGCAGAGC 580
DB 1217 CCAGTCAGAG-----TGAGTAATGATGTAGCTTGTGTACCAACAGAGC 1261
QY 581 CAGGCCAGTCTCCAAAGCTCTCTGATCTACAAAGTTTCCAAACCGATTTTCTGGGGTCCAG 640
DB 1262 CAGGGCAGTCTCTACACTGCTCATATCTCTATACATCCAGTCGCTAGCGTGGAGTCCCTG 1321
QY 641 ACAGTTTCAGTGGCAGTGGATCAGGACAGATTTTCACTCAAGATCAAGATCAGCAGAGTGAGG 700
DB 1322 ATCGCTTCATTTGGCAGTGGATATGGGACGATTTTCACTTCCACATCAGCAGTTCGAGG 1381
QY 701 CTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGATCACATGTTCCGTACACGTTTCGGAG 760
DB 1382 CTGAGACCTGGCAGTTTATTTCTGTGACGAAAGTTATTAATTTCTCTCCGACGTTCCGTTG 1441
QY 761 GGGGACCAAGCTGGAATAAAGAA 786
DB 1442 GAGGACCAAGCTGGAATAAATAA 1467
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RESULT 15
US-10-060-585-1
; Sequence 1, Application US/10060585
; Publication No. US20030083290A1
; GENERAL INFORMATION:
; APPLICANT: Kingsman, Alan J.
; APPLICANT: Bebbington, Christopher R.
; APPLICANT: Carroll, Miles W.
; APPLICANT: Ellard, Fiona M.
; APPLICANT: Kingsman, Susan M.
; APPLICANT: Myers, Kevin A.
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: DYOU23.001CP1
; CURRENT APPLICATION NUMBER: US/10/060,585
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 09/445375
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: GB 9711579.4
; PRIOR FILING DATE: 1997-06-04
; PRIOR APPLICATION NUMBER: GB 9713150.2
; PRIOR FILING DATE: 1997-06-20
; PRIOR APPLICATION NUMBER: GB 9714230.1
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: PCT/GB99/03859
; PRIOR FILING DATE: 1999-11-18
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 729
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 514 ScFv
US-10-060-585-1
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Query Match 38.0%; Score 315.4; DB 9; Length 729;
Best Local Similarity 67.9%; Pred. No. 3.4e-91;
Matches 503; Conservative 1; Mismatches 198; Indels 39; Gaps 3;
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QY 67 GCGGTTCAACTCGACGAGTCTGGGCTGAGCTGGTGGAGCCTGGGGCTTCAGTGACGCTG 126
DB 1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATA 60
QY 127 TCCTGCAAGCCTTCGGGCTACACATTTACTGACTATGAAATACACTGGGTGAGGACAGACA 186
DB 61 TCCTGCAAGCCTTCGGTACTTACTGCTACTGCTACTGCTACTGGGTGAAGCAGAGC 120
QY 187 CTGTGCATGGCTCGAATGGATTTGAGCTATTGATCTGAAACTGGTGGTACTGCTCTAC 246
DB 121 CATGGAAGAGAGCTTGAGTGGATTGGACGTAATTAATCTCAATGCTTACTCTCTAC 180
QY 247 AATCAGAAGTTCAAGGACAGAGCCATAGTACTGTAGACAAATCTCCAGCACAGCCTAC 306
DB 181 AACCGAAATTCAGGACAGAGCCATATTAATCTGTAGACAGTCAATCCACCAGCCTAC 240
QY 307 ATGGAGCTCCGAGCCTGACATCTGAAGACTCTGCGCTCTATTACTATACAAGAT---- 361
DB 241 ATGGAGCTCCGAGCCTGACATCTGAGGACTCTGGGCTCTATTACTGTGCAAGATCTACT 300
QY 362 -----GGTTTGAGGACTGGGCGCAAGGAGCTCTGGTCACTGTCTCTGCA 405
DB 301 ATGATTACGAACATATGTTATGGACTACTGGGTCAAGTAACCTCAGTCACCTCTCTCA 360
QY 406 GAGGTAAATCTCAGGACTCTGGCTCCGAATCCAAACCCGGG---ATGTTGTGATGACC 462
DB 361 GGTGTGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGATCTAGTATTGTGATGACC 420
QY 463 CCAAAACCCACTCTCCCTGCTGCTGATCTTGAGATCAAGCCTCCATCTCTTTCAGATCT 522
DB 421 CAGACTCCACATCTCTGCTGTTTCAGCAGGACAGAGGTTTACCATAACCTGCAAGGCC 480
QY 523 AGTCAGAGCCTTTTACACAGTAATGGAATCACTATTTTACATTTGTTACTCTGCAAGGCCA 582
DB 481 AGTCAGAG-----TGAGTAATGATGTAGDTTGGTGGTACCAACAGAGCCA 525
QY 583 GGCCAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCGATTTTCTGGGTCCTCAGAC 642
DB 526 GGGCAGTCTCTACACTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGAT 585
QY 643 AGGTTTCAGTGGCAGTGGATCAGGAGACAGATTTTACACTCAAGATCAGCAGAGTGGAGCT 702
DB 586 CGCTTCATTGGCAGTGGATATGGAGCGGATTTCACTTTCACCATCAGCAGCTTTGAGGCT 645
QY 703 GAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGTTCCGTACACGTTGGAGGG 762
DB 646 GAAAGACCTGGCAGTTTATTTCTGTGACGAAGATTATAATTTCTCTCCGACGTTCCGTGGA 705
QY 763 GGCACCAAGCTGGAATAAATA 783
DB 706 GGCACCAAGCTGGAATAAATA 726
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Search completed: May 17, 2003, 13:39:18
Job time : 117 secs
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Best Local Similarity 74.1%; Pred. No. 2.1e-114; Mismatches 179; Indels 12; Gaps 2;
Matches 547; Conservative 0;

QY 58 GCCTTTGGGGGGTTCAATCGCAGAGTCTGGGCTGAGCTGGTGGAGCCTGGGGCTTCA 117
Db 1 GCCATGGCCAGGTGCGAGTGCAGAGTCAGGGCGCAGCTTGTGGGTGAGGGCCCTCA 60

QY 118 GTGACGTGCTCTCAAGGCTTGGGCTGACATTTTACTGACTATGAATAACACTGGGTG 177
Db 61 GTCAAGTTGTCTGCACAGCTTCTGGCTTCAACATTAAGAGACTACTATATGCACCTGGTG 120

QY 178 AGGCAGACACTGTCATGGCTGGATGGATGGAGCTATTGATCTGAACTGGTGGT 237
Db 121 AAGCAGAGGCTGAACAGGCTGGAGTGGATGGATGGATGGATGGATGGATGGAT 180

QY 238 ACTGCTCAATCAGAAAGTTCAAGGACAAGGCCATAGTACTGTAGACAAATCTCCAGC 297
Db 181 ACTGAATATGCCCGAAGTTCCAGGCAAGCCACTATGACTGCAGACACATCTCCAAT 240

QY 298 ACAGCTACATGAGCTCGGAGCTGACATCTGAACTCTGCGCTCTATTACTATACA 357
Db 241 ACAGCTACCTGACCTCAGCAGCTGCGATCTGAGGACACTGCGCTCTATTATTGAAT 300

QY 358 AGAT-----GGTTTGAGGACTGGGGCAAGGACTCTGGTCACTGTCTGCGAG 408
Db 301 TTTTACGGGGATGTTTGGACTACTGGGGCAAGGACACCGGTACCGTCTCTCAGGT 360

QY 409 GGTAAATCTCA---GGATCTGGCTCCGAATCCAAACCCGGGATGTTGTGATGACCCCA 465
Db 361 GGAGCGGTTTCAGCGGAGGTGGCTCTGGCGGTGGCGGATCGGATGTTTGTGACCCAA 420

QY 466 AACCACTCTCCCTGCTGCTGAGCTTGGAGATCAAGCTCCATCTCTGCAATCTAGT 525
Db 421 ACTCACTCACTTGTGCGTTTACCATTTGGAACACAGCCCTCCATCTCTGCAAGTCAAGT 480

QY 526 CAGAGCTTTTACACAGTAATGGAATCACTTATTTATGTTGGTACCTGCAGAGCCAGGC 585
Db 481 CAGAGCTCTTGGATGATGATGGAAGACATATTTGATTTGGTTGTACAGAGCCAGGC 540

QY 586 CAGTCTCAAAGCTCTGATCTACAAAGTTTCAACCGATTTTCTGGGGTCCACAGAG 645
Db 541 CAGTCTCAAAGCGCTAATCTATCTGTTGTTAACTGGACTCTGGAGTCCCTGACAGG 600

QY 646 TTAGTGGAGTGCATGAGGACAGATTTACACTCAAGATCAGCAGAGTGGAGCTGAG 705
Db 601 TTAGTGGAGTGCATGAGGACAGATTTACACTCAAGATCAGCAGAGTGGAGCTGAG 660

QY 706 GATCTGGAGTTTATTTCTGCTCTCAAGTACACATGTTCCGTACAGCTTCCGAGGGGG 765
Db 661 GATTTGGAGTTTATTTCTGCTCAAGTACACATTTCTCCGCTCAGCTTCCGTTGGTGG 720

QY 766 ACCAAGCTGGAATAAAA 783
Db 721 ACCAAGCTGAGCTGAAA 738

RESULT 2

US-08-983-035A-37

; Sequence 37, Application US/08983035A

; Patent No. 6326464

; GENERAL INFORMATION:

; APPLICANT: CONSEILLER, EMMANUEL

; BRACCO, LAURENT

; TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL

; DUNNER, LLP

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &

; STREET: 1300 I Street, NW

; CITY: Washington

; STATE: DC

; COUNTRY: USA

ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT: US/08/983,035A
FILING DATE: 20-Feb-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/01111
FILING DATE: 17-JUL-1996
APPLICATION NUMBER: FR 95/08729
FILING DATE: 19-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Strauss, William L.
REGISTRATION NUMBER: 47,114
REFERENCE/DOCKET NUMBER: 03804.0142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 1611 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1605
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-08-983-035A-37

Query Match 48.8%; Score 405.2; DB 4; Length 1611;
Best Local Similarity 74.1%; Pred. No. 1.6e-113;
Matches 544; Conservative 0; Mismatches 178; Indels 12; Gaps 2;

QY 62 TTGGCGGGCTTCAACTGCAGAGTCTGGGGCTGAGCTGGTGGAGCCTGGGGCTTCAAGTGA 121
Db 2 TGGCCAGGTGAGCTGAGGAGTCAGGGCGCAGAGCTTGTGGGTGAGGGGCTCAGTCA 61

QY 122 CGCTGTCCTGCAAGGCTTCGGGCTACACATTTACTGACTATGAAATACACTGGGTGAGGC 181
Db 62 AGTTGCTCTGACAGCTTCTGGCTTCAACATTTAAAGACTACTATATGCACTGGGTGAAGC 121

QY 182 AGACACCTGTCATGGCTGGATGGATGGAGCTATTGATCTGAAACTGGGTGAGTCTG 241
Db 122 AGAGGCTTCAACAGGGCTGGAGTGGATGGATGGATGGATGGATGGATGGATGGATGG 181

QY 242 CCTACAATCAGAAAGTTCAAGGACAGGGCCATAGTACTGTAGACAAATCTCCAGCACAG 301
Db 182 AATATGCCCGAAGTTCCAGGGCAAGGCCACTATGACTGCAGACACATCTCCAATACAG 241

QY 302 CCTACATGAGCTCCGCGAGCTGACATCTGAAAGACTCTCCCGTCTATTACTATACAAGAT 361
Db 242 CCACTCTGAGCTCAGCAGCTGGCATCTGAGGACACTGCGCGTCTATTATTGTAATTTT 301

QY 362 -----GGTTTGAGGACTGGGGCCAGGAGCTCTGGTCACTGTCTCTGCGAGAGGTA 412
Db 302 ACGGGGATGCTTTGGAGTACTTGGGGCCAGGAGCCACCGGTCTCTCCAGGTGGAG 361

QY 413 AATCTCTCA---GGATCTGGCTCCGAATCCAAACCCGGGGATGTGTGATGACCCCAACC 469
Db 362 GCGGTTTCAGGCGAGGTGGCTCTGGGGTGGCGGATCGGATGTTTGTGATGACCCCAACTC 421

QY 470 CACTCTCCCTGCTGCTGAGTCTTGGAGATCAAGCCTCCATCTCTTTCGAGATCTAGTCAGA 529
Db 422 CACTCACTTTGTGGTTTACCAATTGGACAACAGCCTCCATCTCTTTCGAAAGTCAAGTCAGA 481

QY 530 GCCTTTTACACAGTAATGGAATCACTATTATTTACATTTGGTACCTGCAGAGCCAGGCCAGT 589

TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: -
LOCATION: 1..772 /note= "Single-chain antibody fusion protein of B3 monoclonal antibody
OTHER INFORMATION: Variable Heavy chain (V-H) and
OTHER INFORMATION: Variable Light chain (V-L) Fv region
OTHER INFORMATION: joined by a (Gly-4Ser)-3 peptide linker"
FEATURE:
NAME/KEY: CDS
LOCATION: 27..770
US-08-331-397B-33

Query Match 45.8%; Score 380.4; DB 2; Length 772;
Best Local Similarity 72.0%; Pred. No. 3.9e-106;
Matches 533; Conservative 0; Mismatches 186; Indels 21; Gaps 2;
IQY 66 GCGGTTCAACTGCAGCAGTCTGGGGCTGAGCTGGTGAGCGCTGGGGCTTCAGTGACGCT 125
DB 29 GGATGTGAAGCTGGTGAGTCTGGGGGAGCGCTTAGTCAGCGCTGGAGGCTCCCTGAACCT 89
QY 126 GTCTCGCAAGGCTTCGGGCTACACATTTACTGACTATGAATAACACTGGGTGAGGCAGAC 185
DB 89 CTCTGTGCAACCTCTGGATTCACTTCAGTGACTATTACATGTATTGGGTTCGCCAGAC 148
QY 186 ACCTGTGCATGGCTGGAATGGATGGAGCTATTGATCCCTGAAACTGGTGGTACTGCTTA 245
DB 149 TCCAGAGAAGAGCTGGAGTGGGTGGCGATACATTAGTAATGATGATAGTTCCGCCGCTTA 208
QY 246 CAATCAGAAGTTCAAGGACAAGGCCATAGTGACTGTGTAGACAAATCCTCCAGACAGCCTA 305
DB 209 TTGACACTGTAAAGGGCGGTTTCCCATCTCCAGAGACAATGCCAGGAACACCTCTTA 268
QY 306 CATGGAGCTCCGACGCTGACATCTGAAGACTCTGCGGCTCTATTACTATACAAGA----- 360

DB 269 CCTGCAATGAGCGGTCTCAAGTCTTGAGGACACAGCCATATATCTCTGCAAGGACT 328
QY 361 -----TGGTTTGAAGACTGGGGCCAAAGGACTCTGGTCACTGTCTCTGCA-- 405
DB 329 GGCCTGGGAGGCTGTGTTGCTTACTGGGGCCAAAGGACTCTGGTCACTGTCTCTCAGG 388
QY 406 -GAGGTTAAATCTCAGGATCTGGCTCCGAATCCAAATCCAAATCCCGGGGATGTTGTGATGACCCC 464
DB 389 CGAGGCGGATCCGGTGGTGGCGGATCTGGAGTGGCGGAAGGATGTGCTGATGACCCA 448
QY 465 AAACCACTCTCCCTGCTGTGAGTCTTGAGATCAAGCTCCATCTCTTGAGATCTAG 524
DB 449 GTCTCAATTGAGTTTACCTGTGAGTCTTGAGATCAAGCTCCATCTCTTGAGATCTAG 508
QY 525 TCAGAGCCTTTTACACAGTAATGGAATCACTTATTACATTCGTACCTCGCAAGCCAGG 584
DB 509 TCAGATCATTTGACATAGTAATGGAACACCTATTTAGAATGGTACCTCGCAAAACCCAGG 568
QY 585 CCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAAACCGATTTCTGGGGTCCCAGACAG 644
DB 569 CCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAAACCGATTTCTGGGGTCCCAGACAG 628
QY 645 GTTCAGTGGCAGTGGATCAGGACAGATTTACACTCAAGATCAGCAGAGTGGAGGCTGA 704
DB 629 GTTCAGTGGCAGTGGATCAGGACAGATTTACACTCAAGATCAGCAGAGTGGAGGCTGA 688
QY 705 GGATCTGGGAGTTTATTTCTGCTCTCAAGATACACATGTTCCGTACACCTTCGGAGGGG 764
DB 689 GGATCTGGGAGTTTATTTCTGCTCTCAAGATACACATGTTCCATTCACCTTCGGTCCGG 748
QY 765 GACCAAGCTGGAATAAAG 784
DB 749 GACAAAGCTGGAATTAAG 768

RESULT 5

US-08-759-804A-33
Sequence 33, Application US/08759804A
Patent No. 590296
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David J.
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,804A
FILING DATE: 03-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289

Db 766 TATACCTCTCGG---ACGTCGGTGGAGGACCAAGCTCGAGATCAAAACGGGAACAAAA 822

Qy 793 CTACATCTCAGAAGAGGATCTGAATTA 818

Db 823 CTACATCTCAGAAGAAGATCTGAATCA 848

RESULT 8

US-09-227-693-31
; Sequence 31, Application US/09227693
; Patent No. 6287562
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira
; APPLICANT: BENHAR, Itai
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: JUNG, Sun-Hee
; APPLICANT: LEE, Byungkook
; TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
; TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,693
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/331,396
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-126-1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 741 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..741
; OTHER INFORMATION: /note= "Sequence encoding humanized
; Patent No. 6287562
; OTHER INFORMATION: B3 (Fv)"
US-09-227-693-31

Query Match 42.0%; Score 349; DB 4; Length 741;
Best Local Similarity 69.4%; Pred. No. 1.4e-96;
Matches 513; Conservative 0; Mismatches 205; Indels 21; Gaps 2;

Qy 66 GCGCGTTCACTGACGAGCTGGGGCTGAGCTGGTGGAGGCTGGGGCTTCAGTGAGCT 125

Db 3 GCGATGTGAAGCTGGTGGAGCTGGGGGGAGGCGCTGCTGACGCCCGCGCTCCCTGAAACT 62

Qy 126 GTCTGTCAAGCTTCGGGCTACACATTTACTGACTATGAAATACACTGGGTGAGGCAGAC 185
Db 63 CTCTGTGCAACCTCTGGATTCACTTTTCAGTGACTATTACATGTATTGGGTTCGCCAGGC 122
Qy 186 ACCTGTGCATGGCCTGGAATGGATTGGAGCTATTGATCCCTGAAACCTGGTGTACTGCTTA 245
Db 123 CCGGGCAAGGCGCTGGAGTGGGTCCATATAGTAATAGTAGTAGTTCGCGCGCTTA 182
Qy 246 CAATCAGAAGTTTCAAGSACAAAGCCCATAGTACTGTAGACAAATCTCCAGCACAGCCTA 305
Db 183 TTCAGACACTGTAAAGGCGGTTTCAACCATCTCTAGAGACAAAGCAAGAACACCCCTCTA 242
Qy 306 CATGGAGCTCCGAGCCTGACATCTGAAGACTCTGCGGTCTATTACTATATACAAGA----- 360
Db 243 CTGCAAAATGAACCGTCTGCGCGCCGAGGACACAGCCATATATTCCTGTGCAAGAGGACT 302
Qy 361 -----TGGTTTGAGGACTGGGGCCCAAGGACTCTGGTCACTCTCTCTGCA-- 405
Db 303 GGCTGGGAGCCTGGTTTCTTACTGGGGCCCAAGGACTCTGGTCACTCTCTCTCTCAGG 362
Qy 406 -GAGGTTAAATCTCAGGATCTGGCTCCGAATCCAAACCCGGGATGTTGTGATGACCCC 464
Db 363 CGGAGGCGGATCCGTTGGTGGCGGATCTGGAGTGGCGGAAGCGATGTCTGATGACCCA 422
Qy 465 AAACCCACTCTCCCTGCTCTAGTCTTGGAGATCAAGCCTCCATCTCTTCGAGATCTAG 524
Db 423 GTCTCCATTGAGTTTACCTGTCAACCCCGGAGAGCGCGCTCCATCTCTTCGAGATCTAG 482
Qy 525 TCAGAGCCTTTTACAGAGTAATGGAATCCACTTATTTACATTTGGTACCTGCAGAGCCAGG 584
Db 483 TCAGATCATTTGATAGTAATGGAACACCTATTTAGAATGGTACCTGCAGAAACAGG 542
Qy 585 CCAGTCTCCAAAGCTCCTGATCTACAAAGTTTCCAAACCGATTTTCTGGGTCCAGACAG 644
Db 543 CCAGTCTCCACAGCTGCTGATCTACAAAGTTTCCAAACCGATTTTCTGGGTCCAGACAG 602
Qy 645 GTTCAGTGGCAGTGGATCAGGAGACAGATTTACACTCAAGATCAGCAGAGTGGAGGCTGA 704
Db 603 GTTCAGTGGCAGTGGATCAGGAGACAGATTTACACTCAAGATCAGCAGAGTGGAGGCTGA 662
Qy 705 GGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGTTCCCGTACACGTTTCGGAGGGG 764
Db 663 GGACGTGGGAGTTTATTTCTGCTCTCAAGTACACATGTTCCAGGTTTCATGTTCCATTCGCGCAGG 722
Qy 765 GACCAAGCTGCAAAATAAAA 783
Db 723 TACCAAGTCAAAATTAAA 741

RESULT 9

US-08-331-398A-31
; Sequence 31, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: FitzGerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pal, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible


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/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/331,398A
/ FILING DATE: 28-OCT-1994
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/767,331
/ FILING DATE: 30-SEP-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/596,289
/ FILING DATE: 12-OCT-1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hunter, Tom
/ REGISTRATION NUMBER: 38,498
/ REFERENCE/DOCKET NUMBER: 015280-126110US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 543-9600
/ TELEFAX: (415) 543-5043
/ INFORMATION FOR SEQ ID NO: 31:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 738 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
/ FEATURE:
/ NAME/KEY: -
/ LOCATION: 1..738
/ OTHER INFORMATION: /note= "Humanized B3 single-chain Fv"
/ US-08-331-398A-31

Query Match 42.0%; Score 348.2; DB 1; Length 738;
Best Local Similarity 69.5%; Pred. No. 2.4e-96;
Matches 511; Conservative 0; Mismatches 203; Indels 21; Gaps 2;

QY 70 GTTCAACTGCAGCAGTCTGGGGCTGAGCTGGTGGAGGCTGGGGCTTCAGTGGAGCTGTCC 129
DB 4 GTGAAGCTGTGGAGTCTGGGGAGGGCTGCTGCAGCCGGGGCTCCCTGAAACTCTCC 63
QY 130 TGCNAGGCTTGGGCTACATTTACTGACTATCAATACACTGGGTGAGGCAGACCT 189
DB 64 TGTCAACCTCTGGATTCATTTTCAGTGACTATTACATGATTGGGTTCGCCAGGCCCG 123
QY 190 GTGCATGGCTGGAATGGATTGGAGCTATTGATCCTGAAACTGGTGTGCTGCTACAAT 249
DB 124 GGCAAGGCTTGGAGTGGTGGCAGATAGTAGTATGATAGTATGCTGGCGCTTATCA 183
QY 250 CAGAAGTTCAAGGACAAAGGCCATAGTACTGTAGCAAAATCTCCAGCAGCCTCATG 309
DB 184 GACACTGTAAGGCGCGGTTCCACCATCTCTAGAGACAATAGCAAGAACACCCCTCTACCTG 243
QY 310 GAGCTCCGACGCTGACATCTGAGACTCTGGCTCTTACTACTATACAAGA----- 360
DB 244 CAATGAACCGTCTGCCGCGGAGGACACAGCCATATATTCCTGTGCAAGAGGACTGGCC 303
QY 361 -----TGGTTGAGGACTGGGGCAAGGAGCTGTGCTACTGTCTGCA---GAG 408
DB 304 TGGGAGCCTGGTTTGTCTTACTGGGCGCAAGGAGCTGTGCTACTGTCTCTCAGCGGA 363
QY 409 GGTAAATCTCAGAGATCTGGCTCGGAATCCAAACCCGGGATGTTGTGATGACCCCAAC 468
DB 364 GCGGATCCGGTGTGGCGCATCTGGAGGTGGCGGAAGCATGTGCTGATGACCCAGTCT 423
QY 469 CCACTCTCCCTGCTGTGCTGTGGAGATCAAGCTCCATCTCTTCAGATCTAGTCAG 528
DB 424 CCATTGAGTTTACCTGTGACCCCGGGAGAGCCGGCTCCCATCTCTTCAGATCTAGTCAG 483
QY 529 AGCCTTTTACACAGTAATGGAATCACCTATTATGATGGTACTGCAAGAGCCAGGCCAG 588
DB 484 ATCATTTGACATAGTAATGNAACACCTATTATGATGGTACTGCAAGAACCCAGGCCAG 543
QY 589 TCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCGGATTTTCTGGGGTCCCGAGAGGTTCC 648
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DB 544 TCTCCACAGCTGTGATCTACAAAGTTTCCAAACCGATTTCTGGGTCCACAGAGTTC 603
QY 649 AGTGGCAGTGGATCAGGACAGATTTTCACACTCAAGATCAGCAGAGTGGAGGCTGAGGAT 708
DB 604 AGTGGCAGTGGATCAGGACAGATTTTCACACTCAAGATCAGCAGAGTGGAGGCTGAGGAC 663
QY 709 CTGGGAGTTTATTTCTGCTCTCAAAAGTACACATGTTCCGTACACGTTTCGAGAGGGGACC 768
DB 664 GTCCGAGTTTATTTACTGCTTCAAGGTTCCATGTTCCATTCAGCTTCGCGCAGGTACC 723
QY 769 AAGCTGGAATAAAA 783
DB 724 AAGTCAAAATAAAA 738

RESULT 10
US-08-331-397B-31
; Sequence 31, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,397B
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..738
; OTHER INFORMATION: /note= "Humanized B3 single-chain Fv"
; US-08-331-397B-31

Query Match 42.0%; Score 348.2; DB 2; Length 738;
Best Local Similarity 69.5%; Pred. No. 2.4e-96;
Matches 511; Conservative 0; Mismatches 203; Indels 21; Gaps 2;
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QY 529 AGCTTTTACACAGTAATGAATCACCTATTATTTACATTGGTACCTGCAGAACCCAGGCCAG 588
Db 484 ATCAATTGTACATAGTAATGGAACACACCTATTAGAAATGGTATGCTGCAGAAACCCAGGCCAG 543
QY 589 TCTCCAAAGCTCTCTGATCTACAAAGTTTCCAAACCGATTCTTCTGGGGTCCAGACAGGTTTC 648
Db 544 TCTCCAGCTGCTGATCTACAAAGTTTCCAAACCGATTCTTCTGGGGTCCAGACAGGTTTC 603
QY 649 AGTGGCAGTGGATCAGGACAGATTTTCCAACTCAAGATCAGCAGAGTGGAGGCTTGAGGAT 708
Db 604 AGTGGCAGTGGATCAGGACAGATTTTCCAACTCAAGATCAGCAGAGTGGAGGCTTGAGGAT 663
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Db 664 GTCGGAGTTTATTTCTGCTCTCAAGTTCACATGTTCCATTTACGTTTCGGCCAGGGTACC 723
QY 769 AAGCTGGAATAAAAA 783
Db 724 AAGGTGCAATTAATA 738

RESULT 12
US-09-070-637-19
; Sequence 19, Application US/09070637A
; Patent No. 6132722
; GENERAL INFORMATION:
; APPLICANT: SIEMENS, NATHAN O.
; APPLICANT: YARNOLD, SUSAN
; APPLICANT: SENTER, PETER D.
; TITLE OF INVENTION: RECOMBINANT ANTIBODY-ENZYME FUSION PROTEINS
; FILE REFERENCE: 9197F-83-1
; CURRENT APPLICATION NUMBER: US/09/070, 637A
; CURRENT FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: 60/045,888
; EARLIER FILING DATE: 1997-05-07
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
; OTHER INFORMATION: sequence for L49-sfv-bl including PeIB leader.

US-09-070-637-19

Query Match 41.9%; Score 347.4; DB 3; Length 2010;
Best Local Similarity 69.3%; Pred. No. 6.6e-96;
Matches 534; Conservative 0; Mismatches 201; Indels 36; Gaps 3;

QY 46 GCGGCGCATTCCTCGTTGGCGGTTCAACTCAGCAGTCTGGGCTGAGCTGGTGAGG 105
Db 137 GCTGCCAGCGCGGATGGCGAGGTGCGAGTTTCAGAGTTCAGGACCTAGCCTCGTGAA 196
QY 106 CTGGGGCTTCAGTGAAGCTCTCTGCAAGGCTTCGGGTACACATTTACTGACTATGAA 165
Db 197 CCTTCTCAGACTCTGCTCCCTCACTGTTGTGCTGCGGACTTCCATCAGTGGTTAC 256
QY 166 ATACACTGGGTGAGGACAGCACCTGTGCAATGGCTCGAATGATCGAGCTATTGATCT 225
Db 257 TGGAACTGATCGGAAGTTCAGGGAATAAATCTGAAATATATGGTTTACATAGC--- 313
QY 226 GAACTGGTGGTACTGCCTACATCAATCAAGAGTTCAAGGACCAAGCCATAGTACTGTAGAC 285
Db 314 GACAGTGGTATCACTTACTACTAATCCATCTCCTCAAGTTCGCAATTTCCATCACTCGAGAC 373
QY 286 AATCTTCAGACAGCCTACATGGAGTCCGAGCCTGACACTCTGAAAGCTCTGCCGTC 345
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QY 346 TATTACTATACAGATGG-----TTTGAGGACTGGGGCCAGGG 384

Db 434 TATAACTGTGCAAGAGGACTCTGGCTACTTACTATGCTATGGACTACTGGGGTCAAGGA 493
QY 385 ACTCTGTCCTCTCTCTGAGAGGGTAAATCT-----CAGGATCTGGCTCC 432
Db 494 ACCTCTGTACCGTCTCTCAGGCTCGAGCTCGGGTCTGGGCAACCGGGCTCTGGCGAA 553
QY 433 GAATCCAAACCCGGGATGTTGTGATGAGCCCAACCCACTCTCTCTGCTGTGAGTCTTT 492
Db 554 GGCTCTACCAAGGGCGATTGTTGATGAGCCCAAACTCCACTCTCTCTGCTGTGAGTCTTT 613
QY 493 GGAGATCAAGCCTCCATCTCTTGCAGATCTAGTACAGGCTTTTACACAGTAATGAATC 552
Db 614 GGAGATCAAGCCTCCATCTCTTGCAGGCTTAGTACAGGCTTTGATACACAGTAATGAAC 673
QY 553 ACCTATTTACATTTGTTACCTGAGAGGCGGAGCTCTCCAAAGCTCTGATCTACAA 612
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Db 794 TTCACACTCAAGATCAGCAGTGGAGGCTGAGGATCTGGGATTTATTTCTGCTCTCAA 853
QY 733 AGTACACATGTTCCGTTACACGTTTCGGAGGGGAGCCCAAGCTCGAAATAAAA 783
Db 854 AGTACACATGTTCTCCGAGCTTCGGTGGAGGACCAAGCTGGAAATCAA 904

RESULT 13
US-08-752-844-65
; Sequence 65, Application US/08752844
; Patent No. 5935821
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,844
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/DOCKET NUMBER: 30414-20002.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 814 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

FEATURE:
NAME/KEY: CDS
LOCATION: 13..801
US-08-752-844-65

Query Match 40.8%; Score 338.8; DB 2; Length 814;
Best Local Similarity 68.9%; Pred. No. 1.8e-93;
Matches 517; Conservative 0; Mismatches 212; Indels 21; Gaps 3;
QY 55 TCTGCTTTGGCGGTTCAACTGACAGCTCTGGGCTGAGCTGAGGCGCTGGGGCT 114
DB 58 TGTCTCTGTCCTCCAGGTCAGGTCAGGAGTCAGGACCTTTCTCTGGTGGCCCTCACAG 117
QY 115 TCAGTACGCTCTCTCGAAGGCTTCGGCTACACATTTACTGACTACTGAATACATGG 174
DB 118 AGCTGTCCATCAGTACATGCTGTCTGAGGTTCTATTAACCACTATGTTGTAAGCTG 177
QY 175 GTGAGGAGACACCTGTGCTGGCTGGAATGGATTTGGAGCTATTGATCTCTGAAACTGGT 234
DB 178 ATTGCGCAGCTCCAGGAAGGCTCTGAGTGGCTGGGAGCAATTTGGGTGA---CGGG 234
QY 235 GGTACTGCTACAATCAGAAGTTCAAGGACAAGGCCATAGTACTGTAGACAAATCTCTCC 294
DB 235 ACCACAAATTATCATTCAGCTCTCATATCCAGCTGAGCATCAGCAAGGATACTCCAAG 294
QY 295 AGCAGAGCTACATGGAGCTCCGAGCTGACATCTGAAGACTCTGCGCTCTATTACTAT 354
DB 295 AGCCAAGTTTCTTAAACTGAAAGTCTGCAAACTGATGACACGGCCAGCTACTGT 354
QY 355 ACAAGATGG-----TTTGAGACTGGGGCCCAAGGACTCTGGTCACTGTG 399
DB 355 GCCAACTGGGTAAGTACTAGCTCTGAGTACTTGGGTCAGGAACTCAGTCACCGTC 414
QY 400 TCTGACAGGGTAAATCCTCAGGATCTGGCTCCGAATCCAAACCCGG---GGATGTTTG 456
DB 415 TCCTCAGGGGAGGTGCTCGGGCGGTGGGGCTCGGTGGCGCGGATCCGATGTTTG 474
QY 457 ATGACCCCAACCACTCTCCCTGCTGTAGTCTTGGAGATCAAGGCTCTCATCTTGC 516
DB 475 ATGACCAAACTCCACTCTCCCTGCTGTAGTCTTGGAGATCAAGGCTCCATCTCTTGC 534
QY 517 AGATCTAGTCAGAGCTTTTACACAGTAATGGAATCACTTATTTACATTTGATCTCAG 576
DB 535 AGATCTAGTCAGAGCTTTTACATAGTAATGGAACCACTTATTTAGATGATCCTACAG 594
QY 577 AAGCAGGCGAGCTCCAAAGCTCTCATCTCAAAAGTTTCCAAACCGATTTCTTGGGGTC 636
DB 595 AAACCGGCGAGCTCCAAACCTCTCATCTTCTTGTTCCTCAACCGATTTCTTGGGGTC 654
QY 637 CCAGACAGGTTTCAAGCTGAGTGGATCAGGACAGATTTACACTCAAGATCAGCAGAGTG 696
DB 655 CCAGACAGGTTTCAAGCTGAGTGGATCAGGACAGATTTACACTCAAGATCAGCAGAGTG 714
QY 697 GAGGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAAAGTACACATGTTCCGTACAGCTTC 756
DB 715 GAGGCTGAGGATCTGGGAGTTTATTTCTGCTTTCAAGTTTCAATGTTCCGTGACGCTTC 774
QY 757 GGAGGGGGGACCAAGCTGGAATAAAGAA 786
DB 775 GGTGGGAGGACCAAGCTGGAATAAAGAA 804

RESULT 14
US-09-423-439-31
Sequence 31, Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Winthrop, L.L.P.

STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-NOV-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 2019 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-423-439-31

Query Match 40.7%; Score 338.2; DB 4; Length 2019;
Best Local Similarity 70.3%; Pred. No. 4.1e-93;
Matches 524; Conservative 0; Mismatches 188; Indels 33; Gaps 4;
QY 69 GGTCAACTGACAGCTCTGGGCTGAGCTGGTGGGCGCTTGGGCGCTTCACTGAGCTGTC 128
DB 60 GGTCAACTGACAGCTCTGGGCTGAACTGGTGAAGCTTGGGCGCTTCACTGAGCTGTC 119
QY 129 CTGCAAGGCTTGGGCTAGACATTTACTGACTATGAATACACTGGGTGAGGAGACACC 188
DB 120 CTGCAAGGCTTGGGCTAGACCTTCACTGGCTACTGAGTACACTGGGTGAAGGAGGCC 179
QY 189 TGTGATGCGCTGGAATGGATTTGAGCTATTGATCTGAACTGGTGGTACTGCTACAA 248
DB 180 TGGACAAGGCTTGGATGGATTTGAGGAGGTTAATCTAGTACCGGCTTCTGACTACAA 239
QY 249 TCAGAAAGTTCAAGGACAAGGCCATAGTACTGTAGACAAATCTCCAGCACAGCCTACAT 308
DB 240 TGAGAAGTTCAAGAACAGGCCACACTGACTGTAGACAAATCTCCACACAGCCTACAT 299
QY 309 GGAGCTCCGAGCTGACATCTGAAGACTCTGCGGCTTATTTACTATACAAGATGG----- 363
DB 300 GCAACTCAGCAGCTGACATCTGAGGACTCTGCGGCTTATTTACTGTCAAGAGAGAGGC 359
QY 364 -----TTTGAGGACTGGGGCCCAAGGAGCTCTGCTGACTGCTCTCTGC 404
DB 360 CTATGTTTACGAGATGCTATGAGTACTGGGGCCCAAGGAGCCACCGTCACTGCTCTCTC 419
QY 405 A---GAGGGTAAATCTCAGGATCTGGCTCCGAATCCAAACCCGGGGATGTTGTGATGAC 461
DB 420 AGGTGCGGCTGGCTCGGGCGGTGGTGGGTCGGGTGGCGGGATCTGACATTTGAGCTCTC 479
QY 462 CCCAAACCACTCTCCCTGCTGTCAGTCTTGGAGATCAAGCCTTCCATCTCTTTGAGATC 521
DB 480 ACAGTCTCCATCTCTCCCTGGCTGTGTCAGCAGGAGAGAGGTCACCATGAGCTGCAATC 539
QY 522 TAGTCAGAGCTTTTACACAGTAA---TGAATCACCATTATTTACATTGTTGTTGCTGAGAA 578
DB 540 CAGTCAGAGTCTCTCAACAGTAGAACCCGAAAGAACTACTTTGGCTTGGTACAGCAGAG 599
QY 579 GCAGGCCAGTCTCCAAAGCTCTGATCTACAAAGTTTCCAAACCGATTTCTTGGGGTCCC 638
DB 600 ACCAGGGCAGTCTCTTAAGTCTGATCTATTGGGCATCCATAGGACATCTGGGGTCCC 659

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Db 777 TGGAGGCACCAAGCTCGAGATCAA 801

RESULT 15

US-09-423-439-37

Sequence 37, Application US/09423439

Patent No. 6339070

GENERAL INFORMATION:

APPLICANT: EMERY, Stephen Charles

TITLE OF INVENTION: BLAKEY, David Charles

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pillsbury Winthrop, L.L.P.

STREET: 1100 New York Ave., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: MS Word

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/423,439

FILING DATE: 09-No. 6339070-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB98/01294

FILING DATE: 05-MAY-1998

APPLICATION NUMBER: GB 9709421.3

FILING DATE: 10-MAY-1997

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 2025 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

SEQUENCE DESCRIPTION: SEQ ID NO: 37:

IS-09-423-439-37

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Best Local Similarity 70.3%; Pred No. 4,1e-93;
Matches 524; Conservative 0; Mismatches 188; Indels 33; Gaps 4;
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b 60 GGTCCAACTGACAGCAGCCTGGGCTGAACTGGTGAAGCCTGGGGCTTCAGTGACGCTGTC 119
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Job time : 46 secs

GenCore version 5.1.4 p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 16, 2003, 17:41:10 ; Search time 1708 Seconds
(without alignments)
14142.464 Million cell updates/sec

Title: US-09-358-321C-31

Perfect score: 830

Sequence: 1 tctagaatggtgaagcgtcat.....ctgaattagtagcgccgcg 830

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	502.4	60.5	759	12	AJ250763 Mus muscu
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4	499	60.1	753	6	AX003768 Sequence
5	499	60.1	753	6	AX003776 Sequence
6	482.6	58.1	864	12	XXU31739 Single chai
7	476.6	57.4	732	12	XXU44796 Synthetic c
8	476	57.3	792	12	AF276797 Synthetic
9	411.6	49.6	768	6	A57272 Sequence 4
10	409.4	49.3	729	6	BD009689 Anti-p53
11	407.6	49.1	749	6	A59386 Sequence 36
12	407.6	49.1	749	6	ARI79650 Sequence
13	405.2	48.8	1611	6	A59381 Sequence 31
14	405.2	48.8	1611	6	ARI79645 Sequence
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16	397.2	47.9	1101	6	A82599 Sequence 1
17	397.2	47.9	1103	6	A82600 Sequence 2
18	392.8	47.3	795	10	MMSCFVP25 Artificial
19	389.6	46.9	738	10	AF141321 Mus muscu
20	381.6	46.0	925	6	E30617 Antibody an
21	380.4	45.8	772	6	AR085460 Sequence
22	380.4	45.8	772	6	AR088866 Sequence
23	380.4	45.8	772	6	ARI67340 Sequence
24	380.4	45.8	772	6	I36723 Sequence 33
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28	369.4	44.5	720	12	AF059737 Synthetic
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

SCO416563
Synthetic construct partial mRNA for scfv antibody anti-PPV NIB protein.
AJ416563
GI:17978071
anti-PPV NIB protein; antibody; heavy chain; immunoglobulin superfamily; light chain; ScFv; synthetic construct; variable region.
synthetic construct.
synthetic construct
artificial sequences.

753 bp
mRNA
linear
SYN 22-DEC-2001

Esteban,O., Garcia,J.A., Gorris,M.T., Dominguez,E. and Cambra,M.

TITLE Generation and characterization of functional recombinant antibody fragments against RNA replicase Nib from plume pox virus

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 753)

AUTHORS Esteban, O.

TITLE Direct Submission

JOURNAL Submitted (08-OCT-2001) Esteban O., Proteccion Vegetal y Biotecnologia, Inst. Val. Investigaciones Agrarias, CITA. Moncada-Naquera, Km. 4.5, Moncada (Valencia), 46113, SPAIN

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Best Local Similarity 82.4%; Pred. No. 5.3e-145;

Matches 617; Conservative 0; Mismatches 105; Indels 27; Gaps 2;

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62 AGATATCTCGCAAGACTTCTGGATACACATTTCACTGAATACACCATGCACTGGTGAAGC 121

182 AGACACTCTGATGCGCTGGAATGATTGGAGCTATTGATCTCTGAACCTGGTGACTG 241

122 AGAGCATGGAAGAGCCTTGAGTGAATGGAGGTATTAATCTCAACAATGGTGATGA 181

242 CTCAATCAGAAGTTCAAGGCAAGGCCATAGTACTGTAGACAAATCTCCAGCACAG 301

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SC0250763

LOCUS Mus musculus synthetic construct for anti-guinea pig C5 scFv 759 bp mRNA linear SYN 11-MAY-2000

DEFINITION antibody, clone D10.

ACCESSION AJ250763

VERSION AJ250763.1 GI:6272278

KEYWORDS antibody; heavy chain; immunoglobulin superfamily; light chain; scFv; variable region.

SOURCE synthetic construct.

ORGANISM synthetic construct.

REFERENCE 1 (bases 1 to 759)

AUTHORS Link, C., Hawlisch, H., Meyer zu Vilsendorf, A., Gylerez, S., Nagel, E. and Koehl, J.

TITLE Selection of phage-displayed anti-guinea pig C5 or C5a antibodies and their application in xenotransplantation

JOURNAL Mol. Immunol. 36, 1235-1247 (1999)

REFERENCE 2 (bases 1 to 759)

AUTHORS Link, C.

TITLE Direct Submission

JOURNAL Submitted (01-NOV-1999) Link C., Medizinische Mikrobiologie, Medizinische Hochschule Hannover, Carl-Neuberg-Str. 1, 30625 Hannover, GERMANY

FEATURES

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Sequence 17 from Patent WO0003016.
ACCESSION AX006750
VERSION AX006750.1 GI:9994793
KEYWORDS synthetic construct,
SOURCE synthetic construct,
ORGANISM artificial sequences,
REFERENCE 1 (bases 1 to 1637)
AUTHORS Reiter,C.
TITLE Immunological reagent specifically interacting with the
JOURNAL extracellular domain of the human zeta chain
CONEX GMBH (DE); REITER CHRISTIAN (DE)
FEATURES
Location/Qualifiers
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ACCESSION AX003768
VERSION AX003768.1 GI:9927571
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 753)
Kufner, P. and Raum, T.
Method of identifying binding site domains that retain the capacity
of binding to an epitope
Patent: WO 9925818-A 62 27-MAY-1999;
KUFER PETER (DE); RAUM TOBIAS (DE)
FEATURES
source
LOCATION/Qualifiers
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Query Match 60.1%; Score 499; DB 6; Length 753;
Best Local Similarity 81.7%; Pred. No. 1.6e-142;
Matches 615; Conservative 0; Mismatches 105; Indels 33; Gaps 2;
QY 64 GCGCGGTTCACCTGCAGCAGTCTGGGCTGAGCTGTGAGGCTGGGCTTCAGTGAGC 123
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QY 184 ACACCTGTGCATGGCTGGAAATGGATTTGAGTCTCTGAAACTGGTGTGCTGCTGCC 243
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RESULT 5
LOCUS AX003776
DEFINITION Sequence 70 from Patent WO9925818.
ACCESSION AX003776
VERSION AX003776.1 GI:9927575
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 753)
Kufner, P. and Raum, T.
Method of identifying binding site domains that retain the capacity
of binding to an epitope
Patent: WO 9925818-A 70 27-MAY-1999;
KUFER PETER (DE); RAUM TOBIAS (DE)
FEATURES
source
LOCATION/Qualifiers
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/db_xref="taxon:10095"
BASE COUNT 171 a 188 c 215 g 179 t
ORIGIN
Query Match 60.1%; Score 499; DB 6; Length 753;
Best Local Similarity 81.7%; Pred. No. 1.6e-142;
Matches 615; Conservative 0; Mismatches 105; Indels 33; Gaps 2;
QY 64 GCGCGGTTCACCTGCAGCAGTCTGGGCTGAGCTGTGAGGCTGGGCTTCAGTGAGC 123
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QY 184 ACACCTGTGCATGGCTGGAAATGGATTTGAGTCTCTGAAACTGGTGTGCTGCTGCC 243
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QY 394 ACTGTCTCTGCA---GAGGCTAAATCTCTCAGGATCTGCTCCGAATCCAAACCCGGGAT 450
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Db 661 AGAGTGGAGGCTGAGGATCTGGAGTTTATTCTGCTCTCAAGTACACATGTTCCGTAC 720
QY 751 ACGTTCGAGGGGGGACCAAGCTGGAAATAAAA 783
Db 721 ACGTTCGAGGGGGGACCAAGCTTGAGATCAA 753

RESULT 6
XXU31739
LOCUS XXU31739 864 bp DNA linear SYN 05-SEP-1995
DEFINITION Single chain antibody SCA 13.1 gene, complete cds.
ACCESSION U31739
VERSION U31739.1 GI:975304
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
artificial sequences.
REFERENCE
1 (bases 1 to 864)
AUTHORS Nardone,F., Spano,F. and Crisanti,A.
TITLE Direct Submission
JOURNAL Submitted (17-JUL-1995) Francesco Nardone, Istituto di
parasitologia, University of Rome 'La Sapienza', Piazzale Aldo
Moro 5, Roma, RM 00185, Italy
FEATURES
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/db_xref="taxon:32630"
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/notes="single chain antibody derived from monoclonal
antibody against Plasmodium berghiei Pbs21 antigen"
/codon_start=1
/transl_table=11
/product="SCA 13.1"
/protein_id="AAU75173.1"
/db_xref="GI:975305"
/transl_table="MKYLLPTAAAGLLLLAAQPMABEVQOQGAELVRSGASVQLSC
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157..161
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361..393
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BASE COUNT 205 a 222 c 234 g 203 t
ORIGIN
Query Match 58.1%; Score 482.6; DB 12; Length 864;
Best Local Similarity 78.3%; Pred. No. 1.9e-137;
Matches 632; Conservative 0; Mismatches 139; Indels 36; Gaps 3;
QY 46 GCAGCGCATTTCTGCTTTGGCGGTTTCAACTGCAGCAGTCTGGGGCTGAGCTGGTGGG 105
Db 46 GCAGCGCATTTCTGCTTTGGCGGTTTCAACTGCAGCAGTCTGGGGCTGAGCTGGTGGG 105
QY 106 CTTGGGCTTTCACTGAGCGTGTCTTCAAGGCTTTCGGGCTACACATTTACTGACTATGAA 165
Db 106 TCAGGGGCTTCAGTCCAGTTTGTCTGCACAGCTTCTGGCTTCAACATTTAAAGACTTCTAT 165
QY 166 ATACACTGGGTGAGGACAGACCTGTGTCATGGCTGGCTGGAATGGATTGGAGCTATTGATCCT 225
Db 166 ATACACTGGGTGAGGACAGGCGCTGAAACAGGGCTGTGAGTGGATTGGATGATTCCT 225
QY 226 GAAACTGGTGGTACTGCTCAATCAATCAGAAGTTCAAGGACAAAGCCATAGTACTGTAGAC 285
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QY 286 AAATCTCTCCAGCAGCGCTACATGGAGCTCCGAGCGCTGACATCTGAAGACTCTGCCGTC 345
Db 286 ACATCTCTCCAAACAGCGCTACCTGCAGCTCAGCGCGCTGACATCTGGGGACACTGCCGTC 345
QY 346 TATTACTATA-----CAAGATGGTTTGGAGACTGGGGCAAGGG 384
Db 346 TATTCTGTAAATGCTCTAATTTCTACGCTTCTCTCTGCTATGACTACTGGGGCAAGGG 405
QY 385 ACTCTGTCTACTGTCTCTGAGAGGGTAAATCTCA---GGATCTGGCTCCGAATCAAA 441
Db 406 ACCAGGTGACCGTCTCTCTCAGTGGAGCGGTTTCAGGCGGAGGTGGCTCTGGCGGTGGC 465
QY 442 CCGGGGATTTGTGATGACCCCAAAACCCACTCTCCCTGCTGTCTGCTTGGAGATCAA 501
Db 466 GGATCGGATGTTTGTGATGACCCCAAACTCCAATCTCCCTGCTATCAGTCTTGGAGATCAA 525
QY 502 GCCTCCATCTTTGTCAGATCTAGTCAGAGCTTTTACACAGTAATGGAATCACCATTATA 561
Db 526 GCCTCCATCTTTGTAGATCTAGTCAGAGCATTTGTACATAGTAATGGAACACCTATCTA 585
QY 562 CATTGTACCTGTCAGAGCGGCTCTCCAAAGCTCTGATCTACAAAGTTTCCAAAC 621
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QY 622 CGATTTTCTGGGCTCCAGACAGGTTTCAGTGGCAGTGGATCAGGACAGATTTTACACTC 681
Db 646 CGATTTTCTGGGCTCCAGATAGTTTCAGTGGCAGTGGATCAGGACAGATTTTACACTC 705
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QY 790 AAATCATCTCAGAAGAGGATCTGAAT 816
Db 826 AAATCATCTCAGAAGAGGATCTGAAT 852
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RESULT 7
XXU44796          732 bp      mRNA      linear      SYN 03-FEB-1996
LOCUS             Synthetic construct single-chain anti-acetylaminofluorene antibody
DEFINITION        mRNA, from PCR amplified mouse VH and VL regions, partial cds.
ACCESSION         U44796
VERSION           U44796.1
KEYWORDS          GI:1177222
SOURCE            synthetic construct.
                  synthetic construct
                  artificial sequences.
ORGANISM          1 (bases 1 to 732)
                  Guesdon,J.-L. and Muller,B.H.
REFERENCE         Direct Submission
                  Submitted (05-JAN-1996) Jean-Luc Guesdon, Institut Pasteur, 28, rue
                  du Docteur Roux, Paris, 75015, France
JOURNAL
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    BASE COUNT    186 a 182 c 199 g 165 t
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    Query Match    57.4%; Score 476.6; DB 12; Length 732;
    Best Local Similarity 80.6%; Pred. No. 1.3e-135;
    Matches 586; Conservative 0; Mismatches 129; Indels 12; Gaps 2;
    QY 69 GGTTCAACTGCAGCAGTCTGGGGCTGAGCTGGTGAGCGCTTTCAGTGACGCTGTC 128
    DB 3 GGTGCACCTGCAGCAGTCTGGGGCTGAGCTGGCAAAACCTGGGGCCTCAGTGAAGTGC 62
    QY 129 CTGCAAGGCTTCGGGCTACACATTTACTGACTATGAATAACACTGGGTGAGGAGACACC 188
    DB 63 CTGCAAGGCTTCGGCTACACCTTTACTGACTGATGCAATCTGGGTGATGCAAGAGGCC 122
    QY 189 TGTGCATGGCTCGAATGGATTGGAGCTATTGATCTCTGAACTGGTGGTACTGCTTACAA 248
    DB 123 TGGACAGGGCTGGAATGGATTGGATCATTTGATCTCTAGTACTGTTTATTAATTACAA 182
    QY 249 TCAGAAGTTCAAGGACAAGGCCATAGTACTGTAGACAAATCTCTCCAGCAGCAGCTACAT 308
    DB 183 TCAGAAGTTCAAGGACAAGGCCACATTTGATCTGCAGACAAATCTCTCCAGCAGCAGCTACAT 242
    QY 309 GGAGCTCCGAGCCTGACATCTGAAGACTCTGCGCTCTATTACTATACAAG----- 359
    DB 243 GCAACTCAGCAGCCTGACATCTGAAGACTCTGCAAGTCTATTACTGTGCAAGAGGAGACT 302
    QY 360 ATGGTTTGAAGACTTGGGGCCNAGGACTCTGGTCACTGTCTCTGCA---GAGGTTAATC 416
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QY 417 CTGAGGATCTGGCTCCCAATCCAAACCCGGGATGTTGTGATGACCCCAAAACCCACTCTC 476
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QY 477 CTGCGCTGTCACTTTGGAGATCAAGCCTCCATCTCTTGAGATCTTAGTCAGAGCCTTTT 536
DB 423 CTGCGCTGTCACTTTGGAGATCAAGCCTCCATCTCTTGAGGCTCTAGTCAGAGCCTTGA 482
QY 537 ACACAGTAATGGAATCACCTATTATTACATTGGTACCTGCAGAACCCAGGCGAGTCTCCAA 596
DB 483 AACAGTAATGGAACACACCTATTTTGAATGGTACCTCCAGAACCCAGGCGAGTCTCCAA 542
QY 597 GTCCTGTATCTACAAAGTTTCCAAACCGATTTCCTGGGGTCCCAGACAGAGTTTCAGTGGCAG 656
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QY 777 AATAAAA 783
DB 723 GCTGAAA 729

RESULT 8
AF276797          792 bp      mRNA      linear      SYN 02-JUN-2001
LOCUS             Synthetic construct anti-sperm scFv antibody RASA mRNA, partial
DEFINITION        cds.
ACCESSION         AF276797
VERSION           AF276797.1
KEYWORDS          GI:14279759
SOURCE            synthetic construct.
ORGANISM          synthetic construct
                  artificial sequences.
REFERENCE         1 (bases 1 to 792)
                  Norton,E.J., Diekman,A.B., Westbrook,A., Flickinger,C.J. and
                  Herr,J.C.
                  RASA, An Anti-Sperm ScFv Directed Against the Sperm Glycoform of
                  CD52: Implications For Novel Contraceptives
                  Unpublished
                  2 (bases 1 to 792)
                  Norton,E.J., Diekman,A.B. and Herr,J.C.
                  Direct Submission
                  Submitted (09-JUN-2000) Cell Biology, UVA, 2-27 Jordan Hall, 1300
                  Jefferson Park Ave., Charlottesville, VA 22908, USA
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                  and peptide tag"
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Query Match 57.3%; Score 476; DB 12; Length 792;
Best Local Similarity 80.0%; Pred. No. 2e-135;
Matches 592; Conservative 0; Mismatches 130; Indels 18; Gaps 2;

Qy 62 TTGGCGGCTTCACTGAGCAGCTGGGGCTGAGCTGGTGGGCTGGGGCTTCACTGA 121
Db 2 TGGCCAGGTGAAGTCTGAGCAACCTGGGTCTGAACCGGTGAGGCTTGAGCTTCACTGA 61
Qy 122 CGCTGCTCGAAGGCTTTCGGGCTACACATTTACTGACTATCAAAATACACTGGGTGAGGC 181
Db 62 AGGTGCTCTGAGGCTTCTGGCTACAAATTCACACCTACTGGATGCACTGGGTGAGGC 121
Qy 182 AGACACCTGTGCATGGCTGGAATGGATGGAGCTATTGATCCTGAAACTGGGTACTG 241
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Db 362 CGGCGCGCGGAGCGGTGGTGGTCTTGGGGCGCGGAGCGACATCAGAGTCACTC 421
Qy 464 CAAACCCACTCTCCCTGCTCTGAGTCTTGAGATCAAGGCTCCATCTTTGCGAGATCTA 523
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Qy 524 GTCAGAGCTTTTACACAGTAATGAATCACTATTATTCATTTGTTACCTGAGAGCCAG 583
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Qy 704 AGGATCTGGGAGTTTATTCTGCTCTCAAGTACACATGTTCCGTACACGTTCCGAGGGG 763
Db 662 AGGATCTGGGAGTTTATTCTGTTCTCAAGTACACATGTTCCATTCACGTTCCGCTCGG 721
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Db 722 GGACCAAGCTGGAATAAAA 741

RESULT 9
LOCUS A57272 768 bp DNA linear PAT 03-MAR-1998
DEFINITION Sequence 4 from Patent WO9630512.
ACCESSION A57272
VERSION A57272.1 GI:3713167
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

REFERENCE 1 (bases 1 to 768)
AUTHORS Bracco, L., Schweighoffer, F. and Tocque, B.
TITLE CONDITIONAL EXPRESSION SYSTEM
JOURNAL Patent: WO 9630512-A 4 03-OCT-1996;

RHONE POULENC RORER SA (FR)
Other publication AU 5402096 961016
Other publication FR 2732348 961004.
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BASE COUNT 181 a 185 c 218 g 184 t
ORIGIN

Query Match 49.6%; Score 411.6; DB 6; Length 768;
Best Local Similarity 73.9%; Pred. No. 1.5e-115;
Matches 554; Conservative 0; Mismatches 184; Indels 12; Gaps 2;
Qy 46 GCGGCGCATTTCTGCTTTTGGCGGTTCAACTGCGAGCAGTCTGGGGCTGAGCTGGTGAAG 105
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Qy 106 CCTGGGCTTTCAGTGCAGCTGCTCTGCAAGGCTTCGGGCTACACATTTACTGACTATGAA 165
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Db 547 CAGAGCCAGGCGGCTTCCAAAGCGCTTAATCTATCTGCTGCTAAACTGGACTCTGGA 606
Qy 634 GTCCAGACAGAGTTTCAGTGGCAGTGGATCAGGACAGATTTACACTCAAGATCAGAGAGA 693
Db 607 GTCCCTGACAGAGTTTCAGTGGCAGTGGATCAGGACAGATTTACACTTAAATCAACAGA 666
Qy 694 GTGGAGCTGAGGATCTGGGAGTTTATTTCTGCTCTCAAGTACACATGTTCCGTACACG 753
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Qy 754 TTCGAGGGGGGACCAAGCTTGGAAATAAAA 783
Db 727 TTCGCTGCTGCCACCAAGCTTGGAAATAAAA 756

RESULT 10
LOCUS BD009689 729 bp DNA linear PAT 31-JAN-2002
DEFINITION Anti-ps3 single-chain antibody fragments and their uses.
ACCESSION BD009689
VERSION BD009689.1 GI:18638062

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JP 2001502553-A/1.
Spodoptera frugiperda.
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
Noctuoidea; Noctuidae; Amphipyrinae; Spodoptera.
REFERENCE
1 (bases 1 to 729)
AUTHORS
Bracco, L. and Debussche, L.
TITLE
Anti-p53 single-chain antibody fragments and their uses
JOURNAL
Patent: JP 2001502553-A 1 27-FEB-2001;
RHONE POULENC RORER SA
CC
C07K16/18, C12N15/13, A61K39/395
CDS
Key Location/Qualifiers
FT CDS (1)..(729).
FEATURES
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/db_xref="taxon:7108"
BASE COUNT 174 a 171 c 207 g 177 t
ORIGIN
Query Match 49.3%; Score 409.4; DB 6; Length 729;
Best Local Similarity 74.8%; Pred. No. 7.2e-115;
Matches 544; Conservative 0; Mismatches 115; Indels 12; Gaps 2;
QY 69 GGTTCACACTCAGCAGCTCTGGGCTGAGCTGGTGGAGCCCTGGGCTTCAGTGACGCTGTC 128
DB 3 GTGTCAGCTCAGCAGCTCTGGGCGAGAGCTTGTGAGTCAAGGCGCTCAGTCAAGTTGTC 62
QY 129 CTGCAAGCTTCGGGCTACACATTTACTGACTATGAATACACTGGGTGAGGAGACACC 188
DB 63 CTGCACAGCTCTGGCTTCAACATTAAGACTACTATATGCATCTGGGTGAAGCAGAGGCC 122
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DB 183 CCGAAGTTCAGGCGAAGCCACTATGACTGCAGACACATCTCCATACAGCCTACCT 242
QY 309 GGAGCTCCGAGCTGACATCTGAAGACTCTGGCGTCTATTACTATACAGAT- - - - - 361
DB 243 GCAGCTCAGCAGCTCGCATCTCAGGACACTGCGCTCTATTATTGTAATTTTACGGGA 302
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QY 420 A - - - - - GGATCTGGCTCCGAATCCAAACCCGGGGATTTGTGATGACCCCAACCACTCTC 476
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QY 777 AATAAAA 783
Db 723 AATCAAA 729
RESULT 11
LOCUS A59386 749 bp DNA linear PAT 06-MAR-1998
DEFINITION Sequence 36 from Patent WO9704092.
ACCESSION A59386
VERSION A59386.1 GI:3714722
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 749)
AUTHORS Conseller, E. and Bracco, L.
TITLE P53 PROTEIN VARIANTS AND THERAPEUTICAL USES THEREOF
JOURNAL Patent: WO 9704092-A 36 06-FEB-1997;
RHONE POULENC RORER SA (FR)
COMMENT Other publication FR 2736915 970124.
FEATURES
source
1..749
Location/Qualifiers
BASE COUNT 173 a 179 c 221 g 176 t
ORIGIN
Query Match 49.1%; Score 407.6; DB 6; Length 749;
Best Local Similarity 74.1%; Pred. No. 2.6e-114;
Matches 547; Conservative 0; Mismatches 179; Indels 12; Gaps 2;
QY 58 GCCTTTGGCGGCTTCAACTGCAGCAGCTCTGGGCTGAGCTGGTGAAGGCTGGGGCTTCA 117
DB 1 GCATGGCCAGGCTGCAGCTGCAGAGTTCAGGGCAGAGCTTGTGGGTTCAGGGGCTCA 60
QY 118 GTGACGCTGTCTGCAAGCTTCGGGCTACACATTTACTGACTATGAATAACACTGGGTG 177
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QY 178 AGGACAGACCTGTGCTGCTGGCTGGATGGATGGAGCTATTGATCTCTGAACTGGTGT 237
DB 121 AAGCAGAGGCTGAACAGGCGCTGGAGTGGATGGATGATCTCTGAGAATGGTGT 180
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DB 181 ACTGAATATGCCCCGAAGTTCAGGCGCAAGGCGCATATGACTGCAGACACATCTCCAAT 240
QY 298 ACAGCCTACATGGAGCTCCGCGCTGACATCTGAAGACTCTGCCGTCTATTACTATACA 357
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QY 409 GGTAAATCTCA- - - - - GGATCTGCTCCGAATCCAAACCCGGGATGTTGTGATGACCCCA 465
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DB 421 ACTCCACTCACTTTGTGCGTTACCATTTGACAAACAGCCTCCATCTCTTGGCAAGTCAAGT 480
QY 526 CAGAGCCTTTTACAGAGTAAATGGAATCACTATTATCATTTGGTACTCTGCAGAGCCAGGC 585
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Qy 766 ACCAAGCTGGAAATAAAA 783

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RESULT 12

LOCUS AR179650 749 bp DNA linear PAT 20-APR-2002

DEFINITION Sequence 46 from patent US 6326464.

ACCESSION AR179650

VERSION AR179650.1 GI:20221205

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 749)

AUTHORS Conseller, E. and Bracco, L.

TITLE P53 protein variants and Therapeutic uses thereof

JOURNAL Patent: US 6326464-A 46 04-DEC-2001;

FEATURES

Location/Qualifiers

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BASE COUNT 173 a 179 c 221 g 176 t

ORIGIN

Query Match 49.1%; Score 407.6; DB 6; Length 749;

Best Local Similarity 74.1%; Pred. No. 2.6e-114;

Matches 547; Conservative 0; Mismatches 179; Indels 12; Gaps 2;

Qy 58 GCCTTTGGGGGTTCACTGACAGAGTCTGGGGCTGAGCTGGTGAGGCGCTGGGGCTTCA 117

Db 1 GCCATGGCCCGAGTGCAGAGTCAAGGAGTCAGGGCAGAGCTTGTGGGTCAGGGCGCTCA 60

Qy 118 GTGAGCTGTCTCGCAAGCTTTCGGGCTACACATTTACTGACTATGAATAACACTGGGTG 177

Db 61 GTCAGTTGTCTGCACAGCTTCTGGCTTCAACATTAAGACTACTATGACTGGGTG 120

Qy 178 AGGCAGACACCTGTGCATGGCTGGAATGGATTGGAGCTATTGATCTCGAACTGGTGGT 237

Db 121 AAGCAGAGGCTGGAACAGGCTGGAGTGGATTGGATGATTGATCTCGAATGGTGAT 180

Qy 238 ACTGCTACATCAGAAGTTCAAGACAAAGCCATAGTACTGTAGACAAATCTCCAGC 297

Db 181 ACTGAATATGCCCGCAAGTTTCAGGGCAAGGCCACTATGACTGCGACACACATCTCCAAT 240

Qy 298 ACAGCTACATGGAGCTCCGAGCTGACATCTGAAGACTCTGGCGTCTATTACTATACA 357

Db 241 ACAGCTACCTGACAGCTCAGAGCTCGCATCTGAGGACATGCGGCTATTATTGTAAT 300

Qy 358 AGAT-----GGTTGAGGACTGGGGCCCAAGGACTCTGGTCACTGTCTCTGCGAG 408

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Qy 409 GGTAAATCCTCA---GGATCTGGCTCCGAATCCAAACCCGGGGATGTTGTGATGACCCCA 465

Db 361 GGAGCGGTTTACGGCGGAGGTGGCTCTGGCGGTGGCGATCGGATGTTTGTGATGACCCAA 420

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Qy 526 CAGAGCCTTTTACACAGTAATGGAAATCACCTATTATTACATTTGTTACCTGCGAAGCCAGGC 585

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Qy 766 ACCAAGCTGGAAATAAAA 783

Db 721 ACCAAGCTGGAGCTGAAA 738

RESULT 13

LOCUS A59381 1611 bp DNA linear PAT 06-MAR-1998

DEFINITION Sequence 31 from Patent WO9704092.

ACCESSION A59381

VERSION A59381.1 GI:3714713

KEYWORDS

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 1611)

AUTHORS Conseller, E. and Bracco, L.

TITLE P53 PROTEIN VARIANTS AND THERAPEUTICAL USES THEREOF

JOURNAL Patent: WO 9704092-A 31 06-FEB-1997;

COMMENT RHONE POULENC RORER SA (FR)

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BASE COUNT 369 a 443 c 458 g 341 t

ORIGIN

Query Match 48.8%; Score 405.2; DB 6; Length 1611;

Best Local Similarity 74.1%; Pred. No. 1.6e-113;

Matches 544; Conservative 0; Mismatches 178; Indels 12; Gaps 2;

Qy 62 TTGGGGCGGTTCACTGACAGAGTCTGGGGCTGAGCTGGTGAGGCTTGGGGCTTCACTGA 121

Db 2 TGGCCCAAGTGCAGCTGCAGGAGTCAGGGCAGAGCTTGTGGGGTCAGGGCGCTCAGTCA 61

Qy 122 CGCTGTCTCCAAAGGCTTCGGGCTTACACATTTTACTGACTATGAATACACTGGGTGAGGC 181

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DB 722 AGCTGGAGCTGAAA 735

RESULT 14
LOCUS AR179645 1611 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 37 from patent US 6326464.
ACCESSION AR179645
VERSION AR179645.1 GI:20221200
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 1611)
AUTHORS Conseiller,E. and Bracco,L.
TITLE P53 protein variants and therapeutic uses thereof
JOURNAL Patent: US 6326464-A 37 04-DEC-2001;
FEATURES Location/Qualifiers

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/organism="unknown"
BASE COUNT 369 a 443 c 458 g 341 t
ORIGIN

Query Match 48.8%; Score 405.2; DB 6; Length 1611;
Best Local Similarity 74.1%; Pred. No. 1.6e-113;
Matches 544; Conservative 0; Mismatches 178; Indels 12; Gaps 2;

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QY 122 CGCTGCTCTGCAAGGCTTCGGGCTACACATTTTACTGACTATGAAATACACTGGGTGAGGC 181
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DB 482 GCCTCTTGGATAGTAGTGAAGACATATTTGAATTTGGTTGTACAGAGGCCAGGCCAGT 541
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QY 710 TGGGAGTTTATTTCTGCTCTCAAGATCAGATGTTCCGTACAGTTCGGAGGGGGACCA 769
DB 662 TGGGAGTTTATTTCTGCTCAAGATCAGATGTTCCGTACAGTTCGGAGGGGGACCA 721
QY 770 AGCTGGAATAAAAA 783
DB 722 AGCTGGAGCTGAAA 735

AC0131532 729 bp mRNA linear SYN 16-MAR-2000
DEFINITION Synthetic construct for anti-p53 ScFv antibody (scFv421) containing linker sequence.
ACCESSION AJ131532
VERSION AJ131532.1 GI:4033863
KEYWORDS antibody; immunoglobulin superfamily; ScFv; variable region.
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 729)
AUTHORS Caron de Fromental,C., Gruel,N., Venot,C., Debussche,L.,
Conseiller,E., Dureuil,C., Teillaud,J.L., Tocque,B. and Bracco,L.
TITLE Restoration of transcriptional activity of p53 mutants in human
tumour cells by intracellular expression of anti-p53 single chain
Fv fragments
Oncogene 18 (2), 551-557 (1999)
MEDLINE 99124402
PUBMED 9927212

2 (bases 1 to 729)
de Fromental,C.

Direct Submission
Submitted (16-DEC-1998) de Fromental C., U 380 INSERM, Institut

Cochin de Genetique Molculaire, 22 rue Mechain PARIS, 75014,
FRANCE

FEATURES

source

Location/Qualifiers

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BASE COUNT 176 a 168 c 205 g 180 t

ORIGIN

Query Match 48.7%; Score 404.6; DB 12; Length 729;
Best Local Similarity 74.4%; Pred. No. 2.2e-113;
Matches 541; Conservative 0; Mismatches 174; Indels 12; Gaps 2;

Qy 69 GGTTCAACTGCAGCAGTCTGGGGCTGAGCTGGTGGAGGCTTGGGGCTTCAGTGACCGCTGTC 128

Db 3 GGTTCAGCTGCAGCAGTCTGGGGCAGAGCTTGAAGGTGAGGGGCTCAGTCAAGTTGTC 62

Qy 129 CTGCAAGCTTCGGGCTACACATTTACTACTATGAAATACACTGGTGGGAGGAGCACC 188

Db 63 CTGCACAGCTTCGGGCTTCAACATTAAGACTACTATATGCACTGGGTGAAGCAGAGGCC 122

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Db 243 CGAGCTCAGCAGCTGGGCTATCGAGGACACTGCCGTGTTATTGTAATTTTACGGGGA 302

Qy 362 --GGTTTCAGGACTGGGCGCAAGGACTCTGGTCTGTCTCTGAGAGGGTAAATCCTC 419

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Job time : 1717 secs


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Db 268 YTFGGGKLEIK 279

RESULT 2
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DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=COLON;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019760; AAH19760.1;
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;
Query Match 40.1%; Score 558; DB 11; Length 241;
Best Local Similarity 45.6%; Pred. No. 3.2e-41;
Matches 113; Conservative 47; Mismatches 68; Indels 20; Gaps 6;

QY 22 VLQSQGAELVRPGASVTLSCKASGYTFDYEIHWVROTVPVHGLEWIGIDPETGGTAYN 81
Db 2 VLQSQGPPELKKFGETVKISCKASGYTFDYGNNVVKQAPGKGLKMWGINTYTGPTVA 61
QY 82 QKPKDAIVTVKSSSTAYMELSLTSESAVY-----YTRWFEDWGQOTLVTSAGEK 136
Db 62 DDFKGRFAFSLTASTAYLIQINNKNEDATYFCARKOLLRYFDYWGQGTTVTVSSGGG 121
QY 137 SSGSGSEKPG-DVVMTPNPLSPVLSDQASISCRSSQSLHNSGITYLHWYLOKPGQS 195
Db 122 GSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 176
QY 196 PK----LLYKVNRFSGVDRSGSGSGTDFTLKISRVEAEDLGVYFCQSHTVPYTFG 251
Db 177 PRSAHTLHYIQ----PGIPSRFSGSGSGRDSFSISNLEPEDIATYYCLHYDNL-HTFG 231
QY 252 GGTGLEIK 259
Db 232 GGTGLEIK 239

RESULT 3
JBVC16 PRELIMINARY; PRT; 238 AA.
ID JBVC16
AC JBVC16;
Query Match 40.1%; Score 558; DB 11; Length 241;
Best Local Similarity 45.6%; Pred. No. 3.2e-41;
Matches 113; Conservative 47; Mismatches 68; Indels 20; Gaps 6;

QY 22 VLQSQGAELVRPGASVTLSCKASGYTFDYEIHWVROTVPVHGLEWIGIDPETGGTAYN 81
Db 2 VLQSQGPPELKKFGETVKISCKASGYTFDYGNNVVKQAPGKGLKMWGINTYTGPTVA 61
QY 82 QKPKDAIVTVKSSSTAYMELSLTSESAVY-----YTRWFEDWGQOTLVTSAGEK 136
Db 62 DDFKGRFAFSLTASTAYLIQINNKNEDATYFCARKOLLRYFDYWGQGTTVTVSSGGG 121
QY 137 SSGSGSEKPG-DVVMTPNPLSPVLSDQASISCRSSQSLHNSGITYLHWYLOKPGQS 195
Db 122 GSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 176
QY 196 PK----LLYKVNRFSGVDRSGSGSGTDFTLKISRVEAEDLGVYFCQSHTVPYTFG 251
Db 177 PRSAHTLHYIQ----PGIPSRFSGSGSGRDSFSISNLEPEDIATYYCLHYDNL-HTFG 231
QY 252 GGTGLEIK 259
Db 232 GGTGLEIK 239

RESULT 3
JBVC16 PRELIMINARY; PRT; 238 AA.
ID JBVC16
AC JBVC16;
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DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 26.2 kDa protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=COLON;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019760; AAH19760.1;
DR InterPro; IPR003599; IG.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;
Query Match 39.8%; Score 553; DB 11; Length 238;
Best Local Similarity 95.5%; Pred. No. 8.6e-41;
Matches 107; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 148 DVVMTPNPLSPVLSDQASISCRSSQSLHNSGITYLHWYLOKPGQSPKLLIYKVNRF 207
Db 20 DVVMTPNPLSPVLSDQASISCRSSQSLHNSGITYLHWYLOKPGQSPKLLIYKVNRF 79
QY 208 SGVPRFSGSGSGTDFTLKISRVEAEDLGVYFCQSHTVPYTFGGGKLEIK 259
Db 80 SGVPRFSGSGSGTDFTLKISRVEAEDLGVYFCQSHTVPYTFGGGKLEIK 131

RESULT 4
Q925S1 PRELIMINARY; PRT; 218 AA.
ID Q925S1
AC Q925S1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE MRP5 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X., Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium of the irradiated mice by treatment with the intestinal RNA of mice of the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1;
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 2.
DR NON TER 218
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;
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Query Match 38.5%; Score 535.5; DB 11; Length 218;
 Best Local Similarity 49.5%; Pred. No. 2.7e-39;
 Matches 108; Conservative 42; Mismatches 61; Indels 7; Gaps 3;

QY 20 AAVOLQSGAELVRPGASVTLSCKASGYTFTDYEIHVVRQTPVHGLEWIGAIIDPETGGTA 79
 DB 2 AQVKLQSGPELKKPGETVRIKSCASGYTFTAGMQVQKMPGKGLKWIWINTHSGVPK 61

QY 80 YNOKFKDKAIVTVDKSSSTAYMELRLSLTSDSVAVYYTRW-----FEDMGQGTLTVTSAE 134
 DB 62 YABEFGKRTAFSLTASATAYLQISLKNEDTATYFCMRWDYDGGFAYWGQGTITVTSSG 121

QY 135 GKSGSGSGSKPG-DVVMTPNPLSLPVSLGDAQISCRSSQSLHSHNGITYLHWYQLKPG 193
 DB 122 CGSGGGSGSGSDIVLTQSPASLAVSLGORATISCRASES-VDNIGISFMNWFQKPG 180

QY 194 QSPKLLIYKVNRFSGVDPFRFSGSGGTDTFLKISRVE 231
 DB 181 QPKLLIYAASKQSGVGPAGLLASGSGTDFSLNIYPME 218

RESULT 5
 Q99M37 ID Q99M37 PRELIMINARY; PRT; 238 AA.

AC Q99M37; 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 19, Last annotation update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical 26.3 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

QY 216 GSGSGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 259
 DB 61 GSGSGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 104

RESULT 7
 Q9VC55 ID Q9VC55 PRELIMINARY; PRT; 239 AA.

AC Q9VC55; 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 21, Last annotation update)
 DE Hypothetical 26.3 kDa protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

QY 216 GSGSGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 259
 DB 61 GSGSGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 104

Query Match 37.9%; Score 527; DB 11; Length 104;
 Best Local Similarity 96.2%; Pred. No. 5.2e-39;
 Matches 100; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 156 LSLPVSLGDAQISCRSSQSLHSHNGITYLHWYQLKPGSPKLLIYKVNRFSGVDPDRS 215
 DB 1 LSLPVSLGDAQISCRSSQSLHSHNGITYLHWYQLKPGSPKLLIYKVNRFSGVDPDRS 60

QY 216 GSGSGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 259
 DB 61 GSGSGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 104

Query Match 36.3%; Score 505; DB 11; Length 239;
 Best Local Similarity 80.5%; Pred. No. 1.5e-36;
 Matches 95; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 148 DVMTNPLSLPVSLGDAQISCRSSQSLHSHNGITYLHWYQLKPGSPKLLIYKVNRF 207
 DB 20 DVMTNPLSLPVSLGDAQISCRSSQSLHSHNGITYLHWYQLKPGSPKLLIYKVNRF 79

QY 208 SGVDPDRSGSGGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 259
 DB 80 SGVDPDRSGSGGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 131

RESULT 6
 Q9JL82 ID Q9JL82 PRELIMINARY; PRT; 104 AA.

AC Q9JL82; 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

QY 216 GSGSGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 259
 DB 61 GSGSGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 104

Query Match 36.3%; Score 505; DB 11; Length 239;
 Best Local Similarity 80.5%; Pred. No. 1.5e-36;
 Matches 95; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 148 DVMTNPLSLPVSLGDAQISCRSSQSLHSHNGITYLHWYQLKPGSPKLLIYKVNRF 207
 DB 20 DVMTNPLSLPVSLGDAQISCRSSQSLHSHNGITYLHWYQLKPGSPKLLIYKVNRF 79

QY 208 SGVDPDRSGSGGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 259
 DB 80 SGVDPDRSGSGGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 131

RESULT 6
 Q9JL82 ID Q9JL82 PRELIMINARY; PRT; 104 AA.

AC Q9JL82; 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

QY 216 GSGSGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 259
 DB 61 GSGSGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 104

Query Match 37.9%; Score 527; DB 11; Length 104;
 Best Local Similarity 96.2%; Pred. No. 5.2e-39;
 Matches 100; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 156 LSLPVSLGDAQISCRSSQSLHSHNGITYLHWYQLKPGSPKLLIYKVNRFSGVDPDRS 215
 DB 1 LSLPVSLGDAQISCRSSQSLHSHNGITYLHWYQLKPGSPKLLIYKVNRFSGVDPDRS 60

QY 216 GSGSGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 259
 DB 61 GSGSGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 104

Query Match 36.3%; Score 505; DB 11; Length 239;
 Best Local Similarity 80.5%; Pred. No. 1.5e-36;
 Matches 95; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 148 DVMTNPLSLPVSLGDAQISCRSSQSLHSHNGITYLHWYQLKPGSPKLLIYKVNRF 207
 DB 20 DVMTNPLSLPVSLGDAQISCRSSQSLHSHNGITYLHWYQLKPGSPKLLIYKVNRF 79

QY 208 SGVDPDRSGSGGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 259
 DB 80 SGVDPDRSGSGGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 131

RESULT 6
 Q9JL82 ID Q9JL82 PRELIMINARY; PRT; 104 AA.

AC Q9JL82; 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.

QY 216 GSGSGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 259
 DB 61 GSGSGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 104

Query Match 37.9%; Score 527; DB 11; Length 104;
 Best Local Similarity 96.2%; Pred. No. 5.2e-39;
 Matches 100; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 156 LSLPVSLGDAQISCRSSQSLHSHNGITYLHWYQLKPGSPKLLIYKVNRFSGVDPDRS 215
 DB 1 LSLPVSLGDAQISCRSSQSLHSHNGITYLHWYQLKPGSPKLLIYKVNRFSGVDPDRS 60

QY 216 GSGSGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 259
 DB 61 GSGSGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 104

Query Match 36.3%; Score 505; DB 11; Length 239;
 Best Local Similarity 80.5%; Pred. No. 1.5e-36;
 Matches 95; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 148 DVMTNPLSLPVSLGDAQISCRSSQSLHSHNGITYLHWYQLKPGSPKLLIYKVNRF 207
 DB 20 DVMTNPLSLPVSLGDAQISCRSSQSLHSHNGITYLHWYQLKPGSPKLLIYKVNRF 79

QY 208 SGVDPDRSGSGGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 259
 DB 80 SGVDPDRSGSGGTDFTLKISRVEAEDLVYFCQSQTTHVPTFGGGTKLEIK 131

RESULT 6
 Q9JL82 ID Q9JL82 PRELIMINARY; PRT; 104 AA.

AC Q9JL82; 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RN


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RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RE EMBL; AB067793; BAB63278.1; --
DR InterPro: IPR003006; IG_MHC.
FT Pfam; PF00047; ig; 1. 1
FT NON_TER 145 145
FT SEQUENCE 145 AA; 16141 MW; 55A9A7908B2CD6A CRC64;

Query Match 31.6%; Score 439; DB 11; Length 145;
Best Local Similarity 58.4%; Pred. No. 4.8e-31;
Matches 94; Conservative 12; Mismatches 25; Indels 30; Gaps 4;

Qy 22 VOLQSQGAELVPGASVTLSCKASGYTFTDYEHVWVQTPVHGLEWIGALDPETGGTAYN 81
Db 2 VOLQSQGAELVPGASVKLSCKASGYTFTSYMHWVKQPRGRLGRLWIGRIDPNSGCTKYN 61
Qy 82 QKFKDKAIVTVDKSSSTAYMELRLSLSDSAVYYTR-----WFDWGQGLTVTVSAE 134
Db 62 EKFKSKATLTVDKPSSTAYMQLSLTSDSAVYYCARYDYGGSSYFDYWGQGLTVTVS-- 119
Qy 135 GKSSGSGSESKPGDVMTNPVLPVSLDQASISCRSSQS 175
Db 120 -----SESQP-----FNVVPL-----VSCSPLS 139

RESULT 12
Q924P8 PRELIMINARY; PRT; 146 AA.
AC Q924R8;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE VH186-2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RE EMBL; AB067781; BAB63266.1; --
DR InterPro: IPR003006; IG_MHC.
FT Pfam; PF00047; ig; 1.
FT NON_TER 146 146
FT SEQUENCE 146 AA; 16216 MW; 92460F1DFD1B7538 CRC64;

Query Match 31.5%; Score 438.5; DB 11; Length 146;
Best Local Similarity 62.3%; Pred. No. 5.4e-31;
Matches 91; Conservative 14; Mismatches 24; Indels 17; Gaps 3;

Qy 22 VOLQSQGAELVPGASVTLSCKASGYTFTDYEHVWVQTPVHGLEWIGALDPETGGTAYN 81
Db 2 VOLQSQGAELVPGASVKLSCKASGYTFTSYMHWVKQPRGRLGRLWIGRIDPNSGCTKYN 61
Qy 82 QKFKDKAIVTVDKSSSTAYMELRLSLSDSAVYYTR-----WFDWGQGLTVTVSA 133
Db 62 EKFKSKATLTVDKPSSTAYMQLSLTSDSAVYYCARYDYGGSSLYFDYWGQGLTVTVS 121
Qy 134 ECKSGSGSESKPG--DVVMTNPVLPVSLDQASISCRSSQS 157
Db 120 -----SESQP-----FNVVPL-----VSCSPLS 139

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Db 122 E-----SQSPNVFPLVSCSPLS 140

RESULT 13
Q9DBL4 PRELIMINARY; PRT; 473 AA.
AC Q9DBL4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE 1810060009Rik protein.
GN IGH-1 OR 1810060009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamahata I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein W.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
EMBL; AK007918; BAB25349.1; --
DR HSP; P01842; 7FAB
DR MGD; MGI:96443; Igh-1.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig_cl.
DR InterPro: IPR003600; Ig_like.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;

Query Match 31.5%; Score 438; DB 11; Length 473;
Best Local Similarity 52.5%; Pred. No. 3.2e-30;
Matches 95; Conservative 21; Mismatches 45; Indels 20; Gaps 3;

Qy 7 LYVLAAAHSAFAAQLQSQGAELVPGASVTLSCKASGYTFTDYEHVWVQTPVHGLE 66
Db 6 VFLFLLSVTAGVHCQVQLKQSGAELVPGASVKISCKASGYTFTDYINWVKQRPQGLE 65
Qy 67 WIGALDPETGGTAYNOKFKDAIVTVDKSSSTAYMELRLSLSDSAVYYTR-----WF 120
Db 66 WIGKIPGSGSYTAYNOKFKDAIVTVDKSSSTAYMELRLSLSDSAVYYFCARSGDYDWF 125
Qy 121 EDWGGTGLTVTVSAEKGSGS-----GSESKPGDVV--MTPNPLSLPVSLGDOA 166
Db 126 AYWGGTGLTVTVSAAKTAPSYPLAPVCGGTGSSVTLGCLVKGYFPEPVTLTVNWSGSL 185
Qy 167 S 167

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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 481 AA; 52326 MW; 52B44C5826807143 CRC64;

Query Match 31.5%; Score 437.5; DB 11; Length 481;
Best Local Similarity 49.5%; Pred. No. 3.6e-30;
Matches 99; Conservative 23; Mismatches 47; Indels 31; Gaps 7;

QY 7 LVVLAAAHSAFAAVALQOQSGAEILVRPGASVTLCKASGYTFTDYEIHVROTPTVHGLE 66
Db 6 IFELLSGTTGVHSEIQOQSGPELVRPCTSVKVKCKASGYFIDYNIYVVKQSHKKSLE 65

QY 67 WICAIDPETGGTAYNQKFKDKAIVTVDKSSSTAYMELRSLTSEDSAVYY-----YTRWFE 121
Db 66 WIGYIDPYNGSGSSYNQKPKGKATLVTKSSNTAFMYLNNLTSEDSAFYICAREWYCAWFA 125

QY 122 DWGQGLTVTVSAEGKSSGSGSKPGDVVMTNPISLPVSL-GDQASISCRSSQSLLHS- 179
Db 126 FWGQGLTVTVSAE-----SARNP-----TIYPLTLPALSSDPVIOG-----LIHDY 168

QY 180 --NGITYLHWYLOKPGQSPK 197
Db 169 FPGTMNVTV-----GKSGK 183

Search completed: May 16, 2003, 14:25:24
Job time : 88 secs

Db 186 S 186

RESULT 14

Q9UL80 PRELIMINARY; PRT; 114 AA.

AC Q9UL80; (T-EMBLrel. 13, Created)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)

DE Myosin-reactive immunoglobulin light chain variable region (fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

[1]

SEQUENCE FROM N.A.

RP MEDLINE=98277139; PubMed=9614934;

RX Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;

RA "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";

RT Clin. Immunol. Immunopathol. 87:184-192(1998).

RL EMBL; AF035034; AAD56270.1; -.

DR HSSP; P80362; IWL.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_v.

DR Pfam; PF00047; IG; 1.

DR SMART; SM00406; IGV; 1.

FT NON TER 1

FT NON TER 114

SQ SEQUENCE 114 AA; 12775 MW; 070B31E210D1CB01 CRC64;

Query Match 31.5%; Score 437.5; DB 4; Length 114;
Best Local Similarity 76.1%; Pred. No. 4.6e-31;
Matches 86; Conservative 13; Mismatches 13; Indels 1; Gaps 1;

QY 148 DVVMTNPISLPVSLGDPQASISCRSSQSLHSGITYLHWYLOKPGQSPKLLIYKVSNR 207
Db 1 DVMTQSPSLPVTLPQASISCRSSQSPYSDGNTYLVNWFQRPQSPRLIYKVSNRD 60

QY 208 SGVPDRFSGSGGDTFTLKISRVEAEDLGVYFCQSQSTH-VPYTFGGGTGLEIK 259
Db 61 SGVPDRFSGSGGDTFTLKISRVEAEDGVVYCMQGTHTWPPWTFGGGTKEIK 113

RESULT 15

Q8VCV5 PRELIMINARY; PRT; 481 AA.

AC Q8VCV5; (T-EMBLrel. 20, Created)

DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)

DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)

DE Hypothetical 52.3 kDa protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;

[1]

SEQUENCE FROM N.A.

RP TISSUE=MAMMARY TUMOR;

RA Strausberg R.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC018455; AHI18455.1; -.

DR InterPro; IPR003599; IG.

DR InterPro; IPR003597; IG_cl.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_v.

DR Pfam; PF00047; IG; 4.

DR SMART; SM00409; IG; 3.

DR SMART; SM00407; IGcl; 3.

Result No.	Score	Query #		Length	DB	ID	Description
		Match					
1	534	38.4	113	1	KV2G	MOUSE	P01631 mus musculus
2	460	33.1	133	1	KV2F	HUMAN	P06310 homo sapien
3	457	32.9	113	1	KV2D	HUMAN	P01617 homo sapien
4	454	32.6	113	1	KV2E	MOUSE	P03976 mus musculus
5	454	32.6	117	1	KV2E	HUMAN	P06309 homo sapien
6	445.5	32.0	139	1	HV07	MOUSE	P01751 mus musculus
7	436	31.3	112	1	KV2D	MOUSE	P01629 mus musculus
8	435	31.3	113	1	KV2B	HUMAN	P01615 homo sapien
9	431.5	31.0	115	1	KV2A	HUMAN	P01614 homo sapien
10	431.5	31.0	137	1	HV11	MOUSE	P01755 mus musculus
11	423	30.4	138	1	HV48	MOUSE	P03980 mus musculus
12	420	30.2	113	1	KV2F	MOUSE	P01630 mus musculus
13	417.5	30.0	112	1	KV2C	HUMAN	P01616 homo sapien
14	411	29.5	117	1	HV12	MOUSE	P01756 mus musculus
15	411	29.5	117	1	HV13	MOUSE	P01757 mus musculus
16	409	29.4	117	1	HV49	MOUSE	P06328 mus musculus
17	407.5	29.3	118	1	HV51	MOUSE	P06330 mus musculus
18	405.5	29.2	120	1	HV50	MOUSE	P06329 mus musculus
19	405	29.1	117	1	HV09	MOUSE	P01753 mus musculus
20	403	29.0	120	1	HV03	MOUSE	P01747 mus musculus
21	400	28.8	140	1	HV02	MOUSE	P01746 mus musculus
22	393	28.3	136	1	HV10	MOUSE	P01759 mus musculus
23	392	28.2	117	1	HV15	MOUSE	P01754 mus musculus
24	391	28.1	117	1	HV04	MOUSE	P01748 mus musculus
25	388	27.9	113	1	KV2C	MOUSE	P01628 mus musculus
26	383.5	27.6	134	1	KV4C	HUMAN	P06314 homo sapien
27	383	27.5	133	1	KV4B	HUMAN	P06313 homo sapien
28	382.5	27.5	114	1	KV4A	HUMAN	P01625 homo sapien
29	381	27.4	112	1	KV2A	MOUSE	P01749 mus musculus
30	381	27.4	117	1	HV05	MOUSE	P01749 mus musculus
31	381	27.4	117	1	HV14	MOUSE	P01758 mus musculus
32	380	27.3	117	1	HV06	MOUSE	P01750 mus musculus
33	376.5	27.1	108	1	KV1	CANFA	P01618 canis famila

```

RX MEDLINE=74148480; PubMed=4596149;
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
RR "Amino acid sequence of a kappa Bence Jones protein from a case of
RT primary amyloidosis.";
RN Biochemistry 12:3763-3780(1973).
RN [2]
RR SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
RR MEDLINE=73166638; PubMed=4700495;
RR Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
RR Glenner G.G.;
RR "Structural identity of Bence Jones and amyloid fibril proteins in a
RT patient with plasma cell dyscrasia and amyloidosis.";
RT J. Clin. Invest. 52:1276-1281(1973).
CC -!- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
CC WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
CC -!- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A
CC PATIENT WITH PLASMA CELL DYSCRASIA AND AMYLOIDOSIS.
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC PIR: A01888; K2HUTW.
DR DR
DR HSSP; P01607; IREI.
DR InterPro; IPR0031006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Bence-Jones protein; Amyloid.
DR DOMAIN 1 23 FRAMEWORK-1.
FT FT
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT FT
FT DOMAIN 40 54 FRAMEWORK-2.
FT FT
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT FT
FT DOMAIN 62 93 FRAMEWORK-3.
FT FT
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT FT
FT DOMAIN 103 112 FRAMEWORK-4.
FT FT
FT DISULFID 23 93 BY SIMILARITY.
FT FT
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;

Query Match 32.9%; Score 457; DB 1; Length 113;
Best Local Similarity 76.8%; Pred.No. 2.3e-31;
Matches 86; Conservative 13; Mismatches 13; Indels 0; Gaps

QY 148 DVMTPTPLPSVLSDGDAQISCRCSSQSLLHNGITYLHWYLQRPGSPKLLIYKVSNRF 207
DB 1 DIVNTSPLSLVTPTPGPAPASCRCSSQSLLHDGFDYLNWLQRPGSPZLLIYALNSRA 60
QY 208 SGVPDRFGSGSGDTFTLKLSRVEADLGVCFSOSTHVPTFFGGTKLEIK 259
DB 61 SGVPDRFGSGSGDTFTLKLSRVEADVGYTCMALQAQITFGGTRKLEIK 112

RESULT 4
KV2E_MOUSE STANDARD; PRT; 113 AA.
AC P03976;
DD 23-OCT-1986 (Rel. 02, Created)
DDT 23-OCT-1986 (Rel. 02, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 17S29.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI TaxID=10090;
[1]
RR SEQUENCE.
RR TISSUE=Hybridoma;
RR MEDLINE=85128968; PubMed=6441768;
RR "Herbst R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
RR Aebbersold R., Herbszt H., Grutter T., Chang J.Y., Braun D.G.;
RR Muirhead V kappa 25 and V kappa 27 amino-acid sequences of C57B1/6
RT origin: monoclonal antibodies 17S29.1 and 22S25.1 specific for the
RT group A-streptococcal polysaccharide.";
RR Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
CC -!- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
CC PIR: A01912; KVMS17.
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DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 123 93
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12390 MW; 4E93797046F8DB33 CRC64;

Query Match 32.6%; Score 454; DB 1; Length 113;
Best Local Similarity 75.9%; Pred. No. 4.1e-31;
Matches 85; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

QY 148 DVVMTNPPLSLPVSLGDOASISCRSSQLLSHNGITYLHWYLOKPGQSPKLLIYKVSNR 207
DB 1 DIVMTQAVFSPNVLGTSAISCRSSKSLLSHNGITYLWYLOKPGQSPQLLYQMSNLA 60

QY 208 SGVDPDRFSGSGGDTFTLKISRVAEDLGVYFCSTHVPYTFGGGKLEIK 259
DB 61 SGVDPDRFSGSGGDTFTLKISRVAEDGVYCAHNLPLPYTFGGGKLEIK 112

RESULT 5
KV2E HUMAN STANDARD; PRT; 117 AA.
ID -KV2E HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobbeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
diversity.";
RL Nature 309:73-76(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; Z00009; -; NOT ANNOTATED_CDS.
DR PIR; A01889; K2HUGM.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT NON TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 117
FT DOMAIN 5 27
FT DOMAIN 28 43
FT DOMAIN 44 58
FT DOMAIN 59 65
IG KAPPA CHAIN V-II REGION GM607.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.

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FT DOMAIN 66 97
FT DOMAIN 98 106
FT DOMAIN 107 116
FT DISULFID 27 97
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Query Match 32.6%; Score 454; DB 1; Length 117;
Best Local Similarity 77.9%; Pred. No. 4.3e-31;
Matches 88; Conservative 8; Mismatches 17; Indels 0; Gaps 0;

QY 147 GVVMTNPPLSLPVSLGDOASISCRSSQLLSHNGITYLHWYLOKPGQSPKLLIYKVSNR 206
DB 4 GDVMTQSPSLPVTPVTPGEPASISCRSSQLLSHNGYLDWYLOKPGQSPQLLYLGSNR 63

QY 207 FSGVDPDRFSGSGGDTFTLKISRVAEDLGVYFCSTHVPYTFGGGKLEIK 259
DB 64 ASGVDPDRFSGSGGDTFTLKISRVAEDGVYVCMOGLQTPQTFGGGKVEIK 116

RESULT 6
HV07 MOUSE STANDARD; PRT; 139 AA.
ID -HV07 MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region B1-8/186-2 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.B.M., Faskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -! MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
(NPB ANTIBODIES).
CC -----
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CC -----
CC EMBL; J00529; AAA38170.1; -.
DR PIR; A02034; MHMS18.
DR HSSP; P01810; 2FBU.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 139
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DOMAIN 118 124
FT DOMAIN 125 139
FT DISULFID 41 115
FT NON TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC9F465 CRC64;

```

RESULT 8
KV2B_FUMA
ID_KV2B

RL Naturwissenschaften 56:195-205(1969).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
 DR PIR; A01885; K2HUCM.

DR HSSP; P01607; IREI.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DISULFID 24 95 BY SIMILARITY.
 FT NON TER 115 115
 SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 31.0%; Score 431.5; DB 1; Length 115;
 Best Local Similarity 75.2%; Pred. No. 3.1e-29;
 Matches 85; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 148 DVMTPTPLSLPVSIGDQASISCRSSOSLLHS-NGITYLHWYLOKPGOSPKLLIKVSNR 206
 Db 2 DIVMTQTPSLPVTGPGASISCRSSOSLLDSGGNTYLNWYLOKAGOSPLLITLSYR 61

QY 207 FSGVPDRFSGSGGTDFTLKISRVAEADLGVYFCQSQTHVPYTFGGGTGLEIK 259
 Db 62 ASGVPRFSGSGGTDFTLKISRVAEADGVYVCMQRLIEIPYTFGGGTGLEIR 114

RESULT 10
 ID HV11_MOUSE STANDARD; PRT; 137 AA.
 AC P01755;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region S43 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81234548; PubMed=6788376;
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
 RA "Heavy chain variable region contribution to the NPb family of
 RA antibodies: somatic mutation evident in a gamma 2a variable region."
 RL Cell 24:625-637(1981).
 CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
 CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
 CC (NPB ANTIBODIES).
 CC -----
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 CC -----
 CC EMBL; J00539; AAA38172.1; --
 DR PIR; A02038; G2MS43.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
 FT DOMAIN 20 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 FRAMEWORK-3.
 FT DOMAIN 85 85 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 86 117 FRAMEWORK-3.
 FT DOMAIN 118 122 D SEGMENT.
 FT DOMAIN 123 137 JH2 SEGMENT.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON TER 137 137
 SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF4488EC9 CRC64;

Query Match 31.0%; Score 431.5; DB 1; Length 137;
 Best Local Similarity 63.2%; Pred. No. 3.9e-29;
 Matches 86; Conservative 15; Mismatches 28; Indels 7; Gaps 2;

QY 3 SAIVLYVLLAAAHSAFAAVALQOOSGAELVRPGASVTLSCKASGYTFTDYEIHWVROTPV 62
 Db 4 SCIMLF--LAATATGVHSQVLOQOPGAEFVKPGASVKLSCKASGYTFTSYLMHWVNRPG 61

QY 63 HGLEWIGAITDPETGGTAYNQKFKDKAIVTVDKSSSTAYMELRSLTSDSAVYYT----- 117
 Db 62 RGLEWIGRIDPNSGTTYNHFRSKATLTIDKPSSTAYMQLSSLTSDSAVYYCARVLG 121

QY 118 RFPEDWGQGTLTVUSA 133
 Db 122 RYFDYMGQGTTLTVSS 137

RESULT 11
 ID HV48_MOUSE STANDARD; PRT; 138 AA.
 AC P03980;
 DT 23-OCT-1986 (Rel. 02, Created)
 DT 23-OCT-1986 (Rel. 02, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig heavy chain V region TEPC 1017 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=84248078; PubMed=6429663;
 RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
 RA Tucker P.W.;
 RT "Illegitimate recombination generates a class switch from C mu to C
 RT delta in an Igo-secreting plasmacytoma."
 RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
 DR PIR; A02033; HVMST7.
 DR HSSP; P01810; 2FBJ.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; Ig; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
 FT DOMAIN 21 49 FRAMEWORK-1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 68 FRAMEWORK-2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 86 117 FRAMEWORK-3.
 FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 128 138 FRAMEWORK-4.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON TER 138 138
 SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match 30.4%; Score 423; DB 1; Length 138;
 Best Local Similarity 63.5%; Pred. No. 2e-28;
 Matches 87; Conservative 14; Mismatches 28; Indels 8; Gaps 2;

QY 3 SAIVLYVLLAAAHSAFAAVALQOOSGAELVRPGASVTLSCKASGYTFTDYEIHWVROTPV 62
 Db 4 SYILLF--LVATATDVHSQVLOQOPGAELVRPGASVQLSKASGHTFTNYIHWVNRPG 61

QY 63 HGLEWIGAITDPETGGTAYNQKFKDKAIVTVDKSSSTAYMELRSLTSDSAVYY-----Y 116

CCC	-I- MISCELLANEOUS: THE SEQUENCE OF THIS IGM MYELOMA
CCC	CC
CCC	PROTEIN HAS ALSO BEEN DETERMINED.
CCC	-I- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR	PIR, A02039; MMS4E.
DR	HSSP; P01789; IMCP.
DR	InterPro; IPRO03006; Ig_MHC.
DR	InterPro; IPRO03596; Ig_v.
DR	Pfam; PF00047; Ig; 1.
DR	SMART; SM00406; IGv; 1.
KW	Immunoglobulin V region; Glycoprotein.
FT	DISELPTD 22 96 BY SIMILARITY
FT	CARBOHYD 55 55 N-LINKED (GLCNAC..) (COMPLEX).

```
Search completed: May 16, 2003, 14:22:27
Job time : 26 secs
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OM protein - protein search, using sw model

Run on: May 16, 2003, 14:21:35 ; Search time 44 Seconds
(without alignments)
587.731 Million cell updates/sec

Title: US-09-358-321c-32

Perfect score: 1391
Sequence: 1 MVSAILVYVLLAAAHSAFA.....FOGGTKLEIKKEKLISEDL 269

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	748.5	53.8	249	2 S41374	single chain Fv an
2	662.5	47.6	268	2 A56446	Ig heavy chain V r
3	636.5	45.8	233	2 JC5322	p53 specific singl
4	563	40.5	112	2 E27887	Ig kappa chain V r
5	562	40.4	112	2 S32189	Ig kappa chain V r
6	558	40.1	118	2 PT0359	Ig kappa chain V r
7	558	40.1	131	2 B34904	Ig kappa chain pre
8	554	39.8	112	2 D27887	Ig kappa chain V r
9	554	39.8	112	2 S53750	antibody Fab Jel 1
10	554	39.8	115	2 S60066	Ig kappa chain V r
11	554	39.8	131	2 B32513	Ig kappa chain pre
12	554	39.8	131	2 C34904	Ig kappa chain pre
13	552	39.7	111	2 PL0257	Ig kappa chain V r
14	552	39.7	112	2 A27887	Ig kappa chain V r
15	551	39.6	115	2 S38715	Ig kappa chain V r
16	551	39.6	131	2 B30577	Ig kappa chain pre
17	549	39.5	112	2 E27887	Ig kappa chain V r
18	547	39.3	112	2 B31485	Ig kappa chain V r
19	547	39.3	113	2 B41940	Ig light chain V r
20	546	39.3	112	2 C27887	Ig kappa chain V r
21	544	39.1	131	2 C34903	Ig kappa chain pre
22	542	39.0	131	2 D34904	Ig kappa chain pre
23	541	38.9	112	2 A49715	Ig kappa chain V r
24	538	38.7	131	2 PT0178	Ig kappa chain pre
25	537	38.6	131	2 D29380	Ig kappa chain pre
26	534	38.4	113	1 KYMS26	Ig kappa chain V r
27	534	38.4	113	2 PL0205	anti-DNA autoantib
28	534	38.4	132	2 PH0106	anti-digoxin trans
29	534	38.4	219	2 S16112	Ig kappa chain V r

30	531	38.2	131	2 S52449	Ig kappa chain V r
31	529	38.0	112	2 A31807	Ig kappa chain V r
32	527	37.9	131	2 B39276	Ig light chain pre
33	526	37.8	107	2 D32530	Ig kappa chain V r
34	524	37.7	110	2 S26335	Ig kappa chain V r
35	523	37.6	113	2 PL0203	anti-DNA autoantib
36	522	37.5	217	2 S42772	Ig kappa chain - m
37	522	37.5	219	2 S52028	Ig kappa chain - m
38	521	37.5	219	2 PC4203	Ig kappa chain (mo
39	520	37.4	219	2 S38865	Ig kappa chain - m
40	519.5	37.3	130	2 C29380	Ig kappa chain pre
41	519	37.3	112	2 F27887	Ig kappa chain V r
42	513	36.9	112	2 S38719	Ig light chain V r
43	512	36.8	103	2 PH1030	Ig light chain V r
44	512	36.8	108	2 I32530	Ig kappa chain V r
45	510	36.7	114	2 A32967	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

S41374

single chain Fv antibody - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C:Accession: S41374

R:Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A:Description: Construction and functional characterization of a single chain Fv antibody

A:Reference number: S41374

A:Accession: S41374

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-249 <ART>

A:Cross-references: EMBL:229480

Query Match 53.8%; Score 748.5; DB 2; Length 249;

Best Local Similarity 61.1%; Pred. NO. 1.4e-48;

Matches 151; Conservative 29; Mismatches 56; Indels 11; Gaps 3;

QY	22	VOIQQSGAEILVRPGASVTLSCKASGYTFTDYEIHWRVOTPVHGLEWIGAIIDPETGGTAYN	81
DB	2	VOIQQSGAEILVRPGASVKLSCTASGTFNFKDDYIHWRVQKPEKLEWIAIAPASGNVYV	61
QY	82	QKFKDAIVTVDKSSSTAYMELRLTSEDSAVYYTRWTFED-----WGQGTFLVTVSA	133
DB	62	PRQDKATITADTSSNTAYLLSLTSEDTAVYYCAR--RDTLYTSLGYWGQGSTVTVSS	119
QY	134	EGKSSGSGSESKPG-DVVMTPNPLSPVSLGDAQISCRSSQSLHNSNGITYLHWYLOKP	192
DB	120	RGGSGGGGGGGGSDIELTQSPSPVVIIPGESVSIKSKSLXSDGSLYFWFLQRP	179
QY	193	GQSPKLLIYKSNRFGVDPDRFSGSGSGTDFTLKISRVEAEDLGVFCFSOSTHPVPTFGG	252
DB	180	GQSPQLLIYKSNRFGVDPDRFSGSGSGTFTLRISVEAEDGVVYTCMHREYPLTIGA	239
QY	253	GTKLEIK 259	
DB	240	GTKLEIK 246	

RESULT 2

A56446

Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C:Species: Mus musculus (house mouse)

C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996

C:Accession: A56446

R:Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical

A:Reference number: A56446; MUID:95229583; PMID:7713873

A:Accession: A56446

C;Comment: This protein is an anti-double-stranded DNA antibody.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;19-98/Domain: immunoglobulin homology <IMM>

Query Match 40.1%; Score 558; DB 2; Length 118;
Best Local Similarity 95.5%; Pred. No. 8.7e-35;
Matches 107; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 148 DVMTNPPLSLPVSLGDOASISCRSSQSLHNSGITYLHWYLOKPGQSPKLLIYKVSNR 207
DB 4 DVMTQTPPLSLPVSLGDOASISCRSSQSLVHNSGNTYLHWYLOKPGQSPKLLIYKVSNR 63
QY 208 SGVPDRFSGSGGTDFTLKISRVAEDLGIVFCQSOSTHVPVTFGGGKLEIK 259
DB 64 SGVPDRFSGSGGTDFTLKISRVAEDLGIVFCQSOSTHVPVTFGGGKLEIK 115

RESULT 7
B34904
Ig kappa chain precursor V region (12-40 and 5-14) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jul-2000
C;Accession: B34904; H34903
R;Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A;Title: Active site structure and antigen binding properties of idiotypically cross-reactive V region of mouse immunoglobulin V region; immunoglobulin homology
A;Reference number: A34903; MUID:90094387; PMID:2104617
A;Accession: B34904
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA

A;Residues: 1-131 <BED>
A;Cross-references: GB:M32384; GB:J05237; GB:J05238; MID:9639656; PIDN:AAA61589.1; PID:G
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 40.1%; Score 558; DB 2; Length 131;
Best Local Similarity 95.5%; Pred. No. 9.8e-35;
Matches 107; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 148 DVMTNPPLSLPVSLGDOASISCRSSQSLHNSGITYLHWYLOKPGQSPKLLIYKVSNR 207
DB 20 DVMTQTPPLSLPVSLGDOASISCRSSQSLVHNSGNTYLHWYLOKPGQSPKLLIYKVSNR 79
QY 208 SGVPDRFSGSGGTDFTLKISRVAEDLGIVFCQSOSTHVPVTFGGGKLEIK 259
DB 80 SGVPDRFSGSGGTDFTLKISRVAEDLGIVFCQSOSTHVPVTFGGGKLEIK 131

RESULT 8
D27887
Ig kappa chain V region (H36-2) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C;Accession: D27887
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a d
A;Reference number: A91043; MUID:86300656; PMID:2427335
A;Accession: D27887
A;Molecule type: DNA
A;Residues: 1-112 <CAT>

A;Experimental source: strain Balb/c
A;Note: This sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 39.8%; Score 554; DB 2; Length 112;
Best Local Similarity 94.6%; Pred. No. 1.6e-34;
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 148 DVMTNPPLSLPVSLGDOASISCRSSQSLHNSGITYLHWYLOKPGQSPKLLIYKVSNR 207
DB 1 DVMTQTPPLSLPVSLGDOASISCRSSQSLVHNSGNTYLHWYLOKPGQSPKLLIYKVSNR 60

QY 208 SGVPDRFSGSGGTDFTLKISRVAEDLGIVFCQSOSTHVPVTFGGGKLEIK 259
DB 61 SGVPDRFSGSGGTDFTLKISRVAEDLGIVFCQSOSTHVPVTFGGGKLEIK 112

RESULT 9
S53750
antibody Fab Jel 103 light chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jan-2000
C;Accession: S53750
R;Pokkuluri, P.R.; Bouthillier, F.; Li, Y.; Kuderova, A.; Lee, J.; Cygler, M.
J. Mol. Biol. 243, 283-297, 1994
A;Title: Preparation, characterization and crystallization of an antibody Fab fragment t
A;Reference number: S53750; MUID:95018269; PMID:7523684
A;Accession: S53750
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-112 <POK>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 39.8%; Score 554; DB 2; Length 112;
Best Local Similarity 95.5%; Pred. No. 1.6e-34;
Matches 107; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 148 DVMTNPPLSLPVSLGDOASISCRSSQSLHNSGITYLHWYLOKPGQSPKLLIYKVSNR 207
DB 1 DVMTQTPPLSLPVSLGDOASISCRSSQSLVHNSGNTYLHWYLOKPGQSPKLLIYKVSNR 60

QY 208 SGVPDRFSGSGGTDFTLKISRVAEDLGIVFCQSOSTHVPVTFGGGKLEIK 259
DB 61 SGVPDRFSGSGGTDFTLKISRVAEDLGIVFCQSOSTHVPVTFGGGKLEIK 112

RESULT 10
S60066
Ig kappa chain V region (monoclonal antibody C3) (validated) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 23-Feb-1996 #sequence_revision 10-Oct-1997 #text_change 23-Mar-2001
C;Accession: S60066
R;Wien, M.W.; Filman, D.J.; Stura, E.A.; Guillot, S.; Delpeyroux, F.; Crainic, R.; Hogle,
Nat. Struct. Biol. 2, 232-243, 1995
A;Title: Structure of the complex between the Fab fragment of a neutralizing antibody fo
A;Reference number: S60066; MUID:95292109; PMID:7539711
A;Accession: S60066
A;Molecule type: mRNA
A;Residues: 1-115 <WIE>

A;Cross-references: EMBL:X84697; NID:g773226
R;Wien, M.W.; Hogle, J.M.
Submitted to the Brookhaven Protein Data Bank, January 1995
A;Reference number: A52979; PDB:1fpt
A;Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 1-23,'S',25-115
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>
F;23-93/Disulfide bonds: #status experimental

Query Match 39.8%; Score 554; DB 2; Length 115;
Best Local Similarity 95.5%; Pred. No. 1.7e-34;
Matches 107; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 148 DVMTNPPLSLPVSLGDOASISCRSSQSLHNSGITYLHWYLOKPGQSPKLLIYKVSNR 207
DB 1 DVMTQTPPLSLPVSLGDOASISCRSSQSLVHNSGNTYLHWYLOKPGQSPKLLIYKVSNR 60

QY 208 SGVPDRFSGSGGTDFTLKISRVAEDLGIVFCQSOSTHVPVTFGGGKLEIK 259
DB 61 SGVPDRFSGSGGTDFTLKISRVAEDLGIVFCQSOSTHVPVTFGGGKLEIK 112


```
RESULT 11
B32513
IG kappa chain precursor V region (MRL4) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C:Accession: B32513
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n
A:Reference number: A94689; MUID:8831394; PMID:3138286
A:Accession: B32513
A:Molecule type: DNA
A:Residues: 1-131 <KOF>
A:Cross-references: GB:M20828; NID:g196937; PIDN:AAA38843.1; PID:g196938
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 39.8%; Score 554; DB 2; Length 131;
Best Local Similarity 95.5%; Pred. No. 2e-34;
Matches 107; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 148 DVVMTNPPLSLPVSLGDAQISCRSSQSLHNSNGITYLHWYLOKPGQSPKLLIYKVSNR 207
DB 20 DVVMTQTPLSPLVSLGDAQISCRSSQSLVHNSNGNTYLHWYLOKPGQSPKLLIYKVSNR 79
QY 208 SGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSSTHVPYTFGGGKLEIK 259
DB 80 SGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSSTHVPYTFGGGKLEIK 131

RESULT 12
C34904
IG kappa chain precursor V region (3-24) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jan-2000
C:Accession: C34904; I31485
R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A:Title: Active site structure and antigen binding properties of idiotypically cross-reac
A:Reference number: A34903; MUID:90094387; PMID:2104617
A:Accession: C34904
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-131 <BED>
R:Bedzyk, W.D.; Johnson, L.S.; Riordan, G.S.; Voss Jr., E.W.
J. Biol. Chem. 264, 1565-1569, 1989
A:Title: Comparison of variable region primary structures within an anti-fluorescein idi
A:Reference number: A31485; MUID:89109167; PMID:2492278
A:Accession: I31485
A>Status: preliminary
A:Molecule type: protein
A:Residues: 20-52 <BE2>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 39.8%; Score 554; DB 2; Length 131;
Best Local Similarity 94.6%; Pred. No. 2e-34;
Matches 106; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 148 DVVMTNPPLSLPVSLGDAQISCRSSQSLHNSNGITYLHWYLOKPGQSPKLLIYKVSNR 207
DB 20 DVVMTQTPLSPLVSLGDAQISCRSSQSLVHNSNGNTYLHWYLOKPGQSPKLLIYKVSNR 79
QY 208 SGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSSTHVPYTFGGGKLEIK 259
DB 80 SGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSSTHVPYTFGGGKLEIK 131

RESULT 13
B32513
IG kappa chain precursor V region (MRL4) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C:Accession: B32513
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic n
A:Reference number: A94689; MUID:8831394; PMID:3138286
A:Accession: B32513
A:Molecule type: DNA
A:Residues: 1-131 <KOF>
A:Cross-references: GB:M20828; NID:g196937; PIDN:AAA38843.1; PID:g196938
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>

Query Match 39.8%; Score 554; DB 2; Length 131;
Best Local Similarity 95.5%; Pred. No. 2e-34;
Matches 107; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 148 DVVMTNPPLSLPVSLGDAQISCRSSQSLHNSNGITYLHWYLOKPGQSPKLLIYKVSNR 207
DB 20 DVVMTQTPLSPLVSLGDAQISCRSSQSLVHNSNGNTYLHWYLOKPGQSPKLLIYKVSNR 79
QY 208 SGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSSTHVPYTFGGGKLEIK 259
DB 80 SGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSSTHVPYTFGGGKLEIK 131

RESULT 14
A27887
IG kappa chain V region (H37-60) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 21-Jan-2000
C:Accession: A27887
R:Caon, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to a de
A:Reference number: A91043; MUID:86300658; PMID:2427335
A:Accession: A27887
A:Molecule type: DNA
A:Residues: 1-112 <CAT>
A:Experimental source: strain Balb/c
A:Note: This sequence was isolated from the germline gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus he
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 39.7%; Score 552; DB 2; Length 112;
Best Local Similarity 93.8%; Pred. No. 2.3e-34;
Matches 105; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 148 DVVMTNPPLSLPVSLGDAQISCRSSQSLHNSNGITYLHWYLOKPGQSPKLLIYKVSNR 207
DB 1 DVVMTQTPLSPLVSLGDAQISCRSSQSLVHNSNGNTYLHWYLOKPGQSPKLLIYKVSNR 60
QY 208 SGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSSTHVPYTFGGGKLEIK 259
DB 61 SGVPDRFSGSGGTDTFTLKISRVEAEDLGVYFCQSSTHVPYTFGGGKLEIK 111

RESULT 15
S38715
IG kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
```

Search completed: May 16, 2003, 14:26:15
Job time : 45 secs

GenCore version 5.1.4_p5_4578
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DM protein - protein search, using sw model

Run on: May 16, 2003, 14:25:30 ; Search time 68 Seconds
(without alignments)
381.548 Million cell updates/sec

File: US-09-358-321C-32

Perfect score: 1391
Sequence: 1 MVSATVLYVLLAAAHSAFA.....FGGTTKLEIKELISEDL 269

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 362588 seqs, 96450795 residues

Total number of hits satisfying chosen parameters: 362588

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW PUB. pep.*
2: /cgn2_6/ptodata/1/pubpaa/PTCT_NEW PUB. pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW PUB. pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB. pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW PUB. pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB. pep.*
7: /cgn2_6/ptodata/1/pubpaa/PTCTUS_PUBCOMB. pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB. pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW PUB. pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB. pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW PUB. pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB. pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW PUB. pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB. pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	927.5	66.7	252	9 US-09-887-853-4	Sequence 4, Appli
2	823.5	59.2	253	9 US-09-880-748-1964	Sequence 1964, Ap
3	818.5	58.8	260	9 US-09-782-672-2	Sequence 2, Appli
4	793	57.0	331	9 US-10-059-261-169	Sequence 169, App
5	788	56.6	535	9 US-09-968-851-38	Sequence 38, Appli
6	740.5	53.2	281	9 US-10-112-788-9	Sequence 9, Appli
7	730	52.5	258	9 US-10-247-488-4	Sequence 4, Appli
8	730	52.5	260	9 US-09-880-748-1039	Sequence 1039, Ap
9	727	52.3	256	9 US-10-247-488-2	Sequence 2, Appli
10	719	51.7	262	9 US-09-880-748-2081	Sequence 2081, Ap
11	718	51.6	244	9 US-09-880-748-1991	Sequence 1991, Ap
12	709.5	51.0	244	10 US-09-940-391-1	Sequence 1, Appli
13	708	50.9	245	9 US-09-991-470-27	Sequence 27, Appli
14	706.5	50.8	245	9 US-09-880-748-1902	Sequence 1902, Ap
15	706	50.8	248	9 US-09-880-748-1778	Sequence 1778, Ap
16	700.5	50.4	381	10 US-09-822-698A-5	Sequence 5, Appli
17	696	50.0	248	9 US-09-880-748-1104	Sequence 1104, Ap
18	696	50.0	248	9 US-09-880-748-1717	Sequence 1717, Ap
19	696	50.0	250	9 US-09-880-748-932	Sequence 932, App

20 695.5 50.0 239 9 US-10-151-882-23 Sequence 23, Appli
21 695.5 50.0 249 9 US-09-880-748-1635 Sequence 1635, Ap
22 692 49.7 239 9 US-10-162-889-6 Sequence 6, Appli
23 692 49.7 239 10 US-09-808-037-6 Sequence 6, Appli
24 690.5 49.6 243 9 US-09-880-748-2063 Sequence 2063, Ap
25 689 49.5 248 9 US-09-880-748-1733 Sequence 1733, Ap
26 688 49.5 248 9 US-09-880-748-1008 Sequence 1008, Ap
27 687.5 49.4 241 9 US-09-880-748-1948 Sequence 1948, Ap
28 686 49.3 248 9 US-09-880-748-1446 Sequence 1446, Ap
29 685 49.2 248 9 US-09-880-748-1719 Sequence 1719, Ap
30 685 49.2 248 9 US-09-880-748-1737 Sequence 1737, Ap
31 684.5 49.2 245 9 US-09-880-748-1900 Sequence 1900, Ap
32 684.5 49.2 249 9 US-10-237-667-18 Sequence 18, Appli
33 684.5 49.2 249 9 US-10-237-708-18 Sequence 18, Appli
34 684.5 49.2 249 9 US-10-237-866-18 Sequence 18, Appli
35 684.5 49.2 249 9 US-10-237-871-18 Sequence 18, Appli
36 684.5 49.2 249 9 US-10-237-624-18 Sequence 18, Appli
37 684.5 49.2 249 10 US-09-984-186-18 Sequence 18, Appli
38 684 49.2 242 9 US-09-880-748-1580 Sequence 1580, Ap
39 683 49.1 237 10 US-09-924-099-9 Sequence 9, Appli
40 683 49.1 243 10 US-09-924-099-10 Sequence 10, Appli
41 683 49.1 248 9 US-09-880-748-1879 Sequence 1879, Ap
42 682.5 49.1 250 9 US-09-887-853-2 Sequence 2, Appli
43 682.5 49.1 288 10 US-09-818-247-22 Sequence 22, Appli
44 680 48.9 248 9 US-09-880-748-1700 Sequence 1700, Ap
45 679.5 48.8 240 10 US-09-976-787-28 Sequence 28, Appli

ALIGNMENTS

RESULT 1

US-09-887-853-4
Sequence 4, Application US/09887853
Patent No. US20020168375A1
GENERAL INFORMATION:

APPLICANT: Huston, James S.
Oppermann, Hermann
Houston, L. L.
Ring, David B.

TITLE OF INVENTION: Biosynthetic Binding Proteins For Imaging

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/09/887,853

FILING DATE: 21-Jun-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/133,804

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Kelley, Robin D.

REGISTRATION NUMBER: 34,637

REFERENCE/DOCKET NUMBER: 2054/22

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-248-7477

TELEFAX: 617-248-7100

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 252 amino acids

TYPE: amino acid

[illegible]

Query Match 66.7%; Score 927.5; DB 9; Length 252;
Best Local Similarity 76.6%; Pred. NO. 9.2e-51;
Matches 187; Conservative 17; Mismatches 33; Indels 7; Gaps

22 VQLQSSAELVRPGASVLTSCKASGYFTDYEIHWWRQTPVHGLEWIGAIIDPETGCTAYN 81
||||| ||||| :|||: ||||| :|||: ||||| :|||: ||||| :|||: |||||
3 VQLQGSEPLVRPGASVRNSCKSGYIFTDFYMNWRQSHGKSLDYGIVISPSYGVGTGYN 62

```

82 QKFKDAITVDKSSSTAYMELRSLTSDSAVYYY-----TRWFD-WQGTGLTVTSAEG 135
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
63 QKFKGKATLTVDKSSSTAYMELRSLTSDSAVYYYCACSSGNKAMDYWGHGASVTVSSSG 122

```

136 KSSGSGSESKPGDVMTNPPLPSVSLGDAQSISCRSSQSLHNSGITYLHWYLOKPGQS 195
 123 -SSSGSSSSSGSDVMTOTPLPSVSLGDAQSISCRSSQSLVHNSGNTYLNWYLOKAGOS 181

196 PKLLIYKVNRESGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPYTEGGTK 255
|||||
182 PKLLIYKVNRESGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVPYTEGGTK 241
|||||

256 LEIK 259
|||
242 LEIK 245

RESULT 2
IS-09-880-748-1964

Sequence 1964, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Duben et al

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-05-15

PRIOR APPLICATION NUMBER: 60/212,210
 PRIOR FILING DATE: 2000-06-15
 PRIOR APPLICATION NUMBER: 60/240,816
 PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248
 PRIOR FILING DATE: 2001-03-16
 PRIOR APPLICATION NUMBER: 60/277,379
 PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/233,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
COMPLET: 04-04-2004

SEQ ID NO 1964
LENGTH: 253
TYPE: PRT

S-09-880-748-1964

Query Match 59.2%; Score 823.5; DB 9; Length 253;

Y 22 VQLQSGAELVRPGASVTLSCRKASGYTFTDYEIHWVRQTPVHGLEWICAIDPETGGTAYN 81
Matches 164; Conservative 27; Mismatches 47; Indels 13; Gaps

b 2 VQLQSGAEVKEPGASVKVCKASGYTFTSYGISWVRQAPGQGLENNGWISAYNGNTNYA 61

py 82 QKPKDKAIIVTDKSSSTAYMELRSLTSDSAVYYVTR-----WFEDWGQGLTVTV 131

62 QKLQGRVTMTTDTSTAYMELSLRSDDTAVVYCARNPPYYDSSEGFEDYWGOGTMVT 121

132 SAEGKSSGSGSESKPG---DVVMTNPPLSLPVLGPOASISCRSSOSLHSHNGITYLHWY 188

b' 122 SGGGSGGGSGGGSGGSA LDVMTQSP LSLPVT LGQPASISCRSSQLVYSDGNTYL NWF 181

[illegible]

Qy 249 TFGGKLEIK 259
||| ||| : |||
Db 242 TFGQTKMEIK 252

RESULT 3
US-09-782-672-2

sequence 2, Application US/09/82612
Publication No. US20030036092A1
GENERAL INFORMATION:
APPLICANT: Iverson, Brent

Georgiou, George
Chen, Gang
Olsen, Mark J.
Daugherty, Patrick S.

; TITLE OF INVENTION: Directed Evolution of Enzymes and
 ; Antibodies
 ;
 ; NUMBER OF SEQUENCES: 53
 ; CORRESPONDENCE ADDRESS:

ADDRESSEE: ARNOLD, WHITE AND DURKEE
STREET: P.O. Box 4433
CITY: Houston
STATE: TEXAS

COUNTRY: USA
ZIP: 77210-4433
COMPUTER READABLE FORM:

```
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
```

APPLICATION NUMBER: US/09/782,672
FILING DATE: 12-Feb-2001
CLASSIFICATION: <Unknown>

APPLICATION NUMBER: 08/847,063
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: UTSB620
TELECOMMUNICATION INFORMATION:

TELEPHONE: (713) 789-2669
TELEFAX: (713) 789-2679
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-09-782-672-2

Best Local Similarity 66.9%; Fied. NO. 3.5E+4;
Matches 164; Conservative 26; Mismatches 48; Indels 7; Gaps

Db 2 VQLQSGPELVKPGASVPMCKSSGYIFDFYMNWVRQSHCKSLDIYGISPIPSGVGTGIN 61

Qy 82 QKFKDKAIVTVDKSSSTAYMEIRLSLTSBDSAVVY-----TRWFED-WGOGTLVTVSAEG 135

Db 62 QKFKGATLTVDKSSSTAYMELRSLTSEDSAVYYCAGSSGNKWKAMDYWGCHGASVTVSSGG 121

Qv 136 KSSGSGSESKPG-DVVMTPNPISLPVSLGDOASTSCRSSOSLIHSNCITVTHWYLOKPGO 194

Db 122 GSGGGGGGGSDIVLTQSPASLAVSLGQRATISCRSSQSLVHSNGNTYLNWYQQKPGQ 181

195 SPKLLIYKVNRFSGVDPDRFSGSGSDFTLTKISRVEADLGVYFCSQSTHVPYTFGGGT 254
182 PKLLIYKVNRFSGVDPDRFSGSGSDFTLTKISRVEADLGVYFCSQSTHVPYTFGGGT 241
255 KLEIK 259
242 KLELK 246

RESULT 4
US-10-059-261-169
Sequence 169, Application US/10059261
Publication No. US20030077826A1
GENERAL INFORMATION:
APPLICANT: EDELMAN, LENA
APPLICANT: JACOTOT, ETIENNE DANIEL FRANCOIS
APPLICANT: BRIAND, JEAN-PAUL
TITLE OF INVENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET
SPECIFIC CELLS AND A MODULE REGULATING THE APOPTOGENIC
FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX
(PTPC)
FILE REFERENCE: 03495.0216
CURRENT APPLICATION NUMBER: US/10/059,261
CURRENT FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/265,594
PRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 325
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 169
LENGTH: 331
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: vector pAcgp67-ScFv350
peptide sequence
US-10-059-261-169

Query Match 57.0%; Score 793; DB 9; Length 331;
Best Local Similarity 59.2%; Pred. No. 2.6e-42;
Matches 167; Conservative 28; Mismatches 59; Indels 28; Gaps 4;

1 MVSAILVYLLAAAHSAFAA-----VOLQSGAELVPRPGASVTLSC 43
49 MVSAILVYLLAAAHSAFAADLGGSHHHHHIEGREFQVOLQSGAELAKPGASVKLSCK 108
44 ASGYTFDIHVVROTPVHGLEWIGALDPTGTATYNOKEFKDKAIUTVDKSSSTAYMEL 103
109 ASGHTFTSYMMHWVKORPGGLEWIGVYINLSSGYIKYNOEFKDKATLTADKSNATYMH 168
104 RSLTSEDSAVVYTR-----WFDWGOGTLTVSAEKGSGSGSEKPG-DVWMTNPLS 157
169 SLLTSEDSAVVYCARAAQATTFDWGOGTLTVSSGGGGGGGGGGSDIWMQSHKF 228
158 LPVSLGDOASISCRSSQSLHNSGITYLHWYLOKPGOSPKLLIYKVNRFSGVDPDRFSGS 217
229 MSTSVGDRVSITKASQDV-----STAVGWYQKPGOSPKLLIYWASTRITGVDPDRFTGS 283
218 GSGTDFTLTKISRVEADLGVYFCSQSTHVPYTFGGGTLEIK 259
284 GSGTDYTLTSSVQAEADLALYCOQHYSPTPTFGGGLKGIK 325

RESULT 5
US-09-968-851-38
Sequence 38, Application US/09968851
Publication No. US20020193561A1
GENERAL INFORMATION:
APPLICANT: CONSEILLER, EMMANUEL
APPLICANT: BRACCO, LAURENT
TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
USES THEREOF
NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:
ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
DUNNER, LLP
STREET: 1300 I Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/968,851
FILING DATE: 03-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/983,035
FILING DATE: 20-Feb-1998
APPLICATION NUMBER: PCT/FR96/01111
FILING DATE: 17-JUL-1996
APPLICATION NUMBER: FR 95/08729
FILING DATE: 19-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Strauss, William L.
REGISTRATION NUMBER: 47,114
REFERENCE/DOCKET NUMBER: 03804.0142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-09-968-851-38

Query Match 56.6%; Score 788; DB 9; Length 535;
Best Local Similarity 65.2%; Pred. No. 8.4e-42;
Matches 159; Conservative 24; Mismatches 57; Indels 4; Gaps 2;

20 AAVQLQSGAELVPRPGASVTLSCASGYTFTDYEIHWVQTPVHGLEWICADPETGGTA 79
2 AQVQLQSGAELVPRPGASVTLSCASGYTFTDYEIHWVQTPVHGLEWICADPETGGTA 61
80 YNOKFKDKAIUTVDKSSSTAYMELRSLTSEDSAVVY---YTRWFDWGOGTLTVTSAGK 136
62 YAPKFGKATMTADTSSNTAYLQLSLASEDTAVVYCNFYGDALDYWGOGTLTVTSAGG 121
137 SSGSGSEKPG-DVWMTNPLSIPVSLGPDQASISCRSSQSLHNSGITYLHWYLOKPGOS 195
122 GSGGGGGGGGGSDVLTMTQPLTSLVTIGTPASISCKSSQSLDSDGKTYLWMLLQRP 181
196 PKLLIYKVNRFSGVDPDRFSGSGSDFTLTKISRVEADLGVYFCSQSTHVPYTFGGGT 255
182 PKLLIYKVNRFSGVDPDRFSGSGSDFTLTKINRVEADLGVYFCSQSTHVPYTFGGGT 241
256 LEIK 259
242 LELK 245

RESULT 6
US-10-112-788-9
Sequence 9, Application US/10112788
Publication No. US20030077676A1
GENERAL INFORMATION:
APPLICANT: DENARDO, SALLY
APPLICANT: WINTHROP, MICHELLE
APPLICANT: DENARDO, GERALD

```
;; TITLE OF INVENTION: ANTI-MUC-1 SINGLE CHAIN ANTIBODIES FOR TUMOR TARGETING
;; FILE REFERENCE: 309T-000210US
;; CURRENT APPLICATION NUMBER: US/10/112,788
;; CURRENT FILING DATE: 2002-03-28
;; PRIOR APPLICATION NUMBER: US 60/280,721
;; PRIOR FILING DATE: 2001-04-30
;; NUMBER OF SEQ ID NOS: 19
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 9
;; LENGTH: 281
;; TYPE: PRT
;; ORGANISM: Mus musculus
;; US-10-112-788-9

Query Match      53.2%; Score 740.5; DB 9; Length 281;
Best Local Similarity 58.1%; Pred. No. 4.1e-39;
Matches 147; Conservative 32; Mismatches 61; Indels 13; Gaps 3;

QY 14 AAHSFAAVALQSGAELVRPGASVTLSCASGYTFTDYEIHWVROTVPVHGLEWIGAIDP 73
IDB 16 AAQPAMAQVQLQSGTEWVRPGASVTLSCASGYFTSYDIDWVROTPEQGLEWIGWIFP 75

QY 74 ETGCTAYNOKFKDKAIVTVDKSSSTAYMELRLSLTSDSAVY-----YTRWFEDKQGT 127
DB 76 GEGSTEYNEKFKGRATLSVDKSSSTAYMELRLTSLTSDSAVYFCARGDYRRYFDLWQGT 135

QY 128 LVTVAEGKSSGSGSESKPG--DVVMTNPPLSLPVSLGDOASISCRSSQSLHSHNGITYLH 186
IDB 136 TVTVSSRGSGSGSGGSDIELTQSPAIMSASPGERVMTTCSASS-----TRYIY 189

QY 187 WYLOKQCSKPLLIYKVNRFSGVDRFSGSGGTFTLTKISRVEAEDLGVPFCSTHVV 246
IDB 190 WYQOKPGSPRLLIYDTSNVAPGVPRFSGSGGTSLTINRMEADAATYYCQWSGY 249

QY 247 PYTFGGGTGLEIK 259
DB 250 PYTFGGGTGLEIK 262

RESULT 7
US-10-247-488-4
; Sequence 4, Application US/10247488
; Publication No. US2003002244A1
; GENERAL INFORMATION:
; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH &
; TITLE OF INVENTION: SINGLE-CHAIN ANTIBODY AGAINST MUTANT P53
; FILE REFERENCE: 1196336-RAMOT
; CURRENT APPLICATION NUMBER: US/10/247,488
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/526,738
; PRIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Humanus
; US-10-247-488-4

Query Match      52.5%; Score 730; DB 9; Length 258;
Best Local Similarity 59.0%; Pred. No. 1.7e-38;
Matches 144; Conservative 31; Mismatches 59; Indels 10; Gaps 3;

QY 20 AAVQLQSGAELVRPGASVTLSCASGYTFTDYEIHWVROTVPVHGLEWIGAIDPETGGTA 79
DB 2 AQVKLQSGAELAKPGASVMSCKTSGYFTSTWMMVQRPQCGLEWIGYINPTTGYTK 61

QY 80 YNQKFKDKAIVTVDKSSSTAYMELRLSLTSDSAVYYT---RWFEDWGGTTLTVSAEGK 136
DB 62 YNQKFKDKATLTADKSSSTAYMQLSSLTNVDSAVYCTTGYSYFDYWGQTTTVSSGGG 121

QY 137 SSGSGSESKPG--DVVMTNPPLSLPVSLGDOASISCRSSQSLHSHNGITYLHWYLOKPGQS 195
DB 137 SSGSGSESKPG--DVVMTNPPLSLPVSLGDOASISCRSSQSLHSHNGITYLHWYLOKPGQS 195
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DB 122 GSGGGSGGGSDIELTQSPAIMSASPGKVTITCSASS-----VNYMHWFOQKPGTS 175
QY 196 PKLLIYKVNRFSGVDRFSGSGGTFTLTKISRVEAEDLGVPFCSTHVPYTFGGGTGK 255
DB 176 PKLWISSTSNLASGVPARFSGSGGTSLTISRNEADAATYYCQQRSSYPYTFGGGTGK 235
QY 256 LEIK 259
DB 236 LQIK 239

RESULT 8
US-09-880-748-1039
; Sequence 1039, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1039
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-1039

Query Match      52.5%; Score 730; DB 9; Length 260;
Best Local Similarity 57.8%; Pred. No. 1.7e-38;
Matches 149; Conservative 30; Mismatches 59; Indels 20; Gaps 4;

QY 22 VOLQSGAELVRPGASVTLSCASGYTFTDYEIHWVROTVPVHGLEWIGAIDPETGGTAYN 81
DB 2 VOLQSGPEVKKPGSSVKVSCRTSGTFRNYGLSWVRQAPGQGLEWMMGVIPISSTIKYG 61

QY 82 QKFKDKAIVTVDKSSSTAYMELRLSLTSDSAVY-----YTRWF---EDWQO 125
DB 62 QKFDRLTIVADDLTNTTMYMELSLRPEDTAVYYCARAATTSQKHNYAYFYFGDMVMGR 121

QY 126 GTLVTVAEGKSSGSGSESKPG--DVVMTNPPLSLPVSLGDOASISCRSSQSLHSHNGI 182
DB 122 GTITVSSGGSGSGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGG 181

QY 183 TYLHWYLOKPGQSKPLLIYKVNRFSGVDRFSGSGGTFTLTKISRVEAEDLGVPFCSTH 242
DB 182 IYLDWYLOKPGQSKPLLIYKVNRFSGVDRFSGSGGTFTLTKISRVEAEDLGVPFCSTH 241

QY 243 STHVP-YTFGGGTGLEIK 259
DB 242 ALHTPAITFGGTGLEIK 259

RESULT 9
US-10-247-488-2
; Sequence 2, Application US/10247488
; Publication No. US2003002244A1
; GENERAL INFORMATION:
; APPLICANT: RAMOT UNIVERSITY AUTHORITY FOR APPLIED RESEARCH &
; TITLE OF INVENTION: SINGLE CHAIN ANTIBODY AGAINST MUTANT P53
; FILE REFERENCE: 1196336-RAMOT
; CURRENT APPLICATION NUMBER: US/10/247,488
```



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; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1778
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-880-748-1778

Query Match          50.8%; Score 706; DB 9; Length 248;
Best Local Similarity 55.4%; Pred. No. 5.1e-37;
Matches 139; Conservative 34; Mismatches 60; Indels 18; Gaps 3;

QY 22 VLOQSGAELVRPGASVTLSCKASGYFTDYEHVVRQTPVHGLEWIGAIDPETGGTAYN 81
   |||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 2  VLOQSGAEVRKPGASVKVCKASGYFTTSYGISWRQAPGHGLEMMGWISAYNGNTNYA 61
   ||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 82 QKFKDKAIVTVDKSSSTAYMELRSLTSEDGAVVYVYTRWFED-----WGQGTLV 129
   ||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 62 QKQGRVTMTDTSTAYMELRSLRSDDTAVYICARSYYDILTGYPFGMDVWKGKTMV 121
   ||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 130 TVSAEGKSGSGSGSEKPG-DVVMTPNPLSLPVLGDAQSISCRSSQSLHNSGITYLHWY 188
   ||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
Db 122 TVSSGGGGGGGGGGGGSDIQMTQSPSTLSASIGDRVTITCRASEGIYH-----WLAWY 176
   ||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||: :||:
QY 189 LQKPGQSPKLLIYKVSNRFGVDPFRFGSGSGCTDFTLKISRVEAEDLGVYFCQSQSTHPY 248
   |||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 177 QQKPGKAPKLLIYKASSLASGAPRFGSGSGCTDFTLTISLQPDPTATYYCQYSNYPL 236
   |||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
QY 249 TFGGGTKLEIK 259
   |||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:
Db 237 TFGGGTKLEIK 247
   |||||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||: :|||:

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Search completed: May 16, 2003, 14:35:19
Job time : 70 secs

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OM protein - protein search, using sw model

Run on: May 16, 2003, 14:22:00 ; Search time 29 Seconds
(without alignments)
272.923 Million cell updates/sec

Title: US-09-358-321C-32

Perfect score: 1391
Sequence: 1 MVSAILVLYVLLAAAHSAFA.....FGGTTKLEKEKLISEEDL 269

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	928.5	66.8	367	1	US-08-257-341-5 Sequence 5, Appli
2	927.5	66.7	246	1	US-08-257-341-7 Sequence 7, Appli
3	927.5	66.7	252	1	US-08-133-804-4 Sequence 4, Appli
4	927.5	66.7	252	1	US-08-461-838-4 Sequence 4, Appli
5	927.5	66.7	252	2	US-08-461-838-4 Sequence 4, Appli
6	848.5	61.0	269	4	US-09-070-408-132 Sequence 132, App
7	830	59.7	288	4	US-09-423-439-38 Sequence 38, Appli
8	818.5	58.8	260	2	US-08-447-402-1 Sequence 1, Appli
9	806.5	58.0	247	4	US-09-227-693-34 Sequence 34, Appli
10	806.5	58.0	248	1	US-08-331-398A-34 Sequence 34, Appli
11	806.5	58.0	248	1	US-08-331-397B-34 Sequence 34, Appli
12	806.5	58.0	248	2	US-08-759-804A-34 Sequence 34, Appli
13	788.5	56.7	638	4	US-09-070-837-20 Sequence 20, Appli
14	788	56.6	535	4	US-08-983-835A-38 Sequence 38, Appli
15	779.5	56.0	673	4	US-09-423-439-32 Sequence 32, Appli
16	767	55.1	273	2	US-08-403-853-18 Sequence 18, Appli
17	762	54.8	365	3	US-08-875-811-53 Sequence 53, Appli
18	762	54.8	366	3	US-08-875-811-55 Sequence 55, Appli
19	761.5	54.7	281	4	US-09-025-769B-178 Sequence 178, App
20	761	54.7	271	2	US-08-894-922A-10 Sequence 10, Appli
21	755.5	54.3	263	2	US-08-752-844-66 Sequence 66, Appli
22	747	53.7	252	2	US-08-894-922A-14 Sequence 14, Appli
23	742	53.3	239	3	US-08-279-772A-8 Sequence 8, Appli
24	742	53.3	239	4	US-08-902-486-11 Sequence 11, Appli
25	741	53.3	553	2	US-08-263-911-7 Sequence 7, Appli
26	740.5	53.2	483	2	US-08-392-338A-19 Sequence 19, Appli
27	740.5	53.2	483	3	US-09-166-750-19 Sequence 19, Appli

28	740.5	53.2	483	3	US-09-166-093-19	Sequence 19, Appli
29	740.5	53.2	483	3	US-09-172-019-19	Sequence 19, Appli
30	740.5	53.2	483	3	US-09-166-094-19	Sequence 19, Appli
31	740	53.2	553	2	US-08-263-911-9	Sequence 9, Appli
32	739	53.1	289	3	US-09-184-658-63	Sequence 63, Appli
33	739	53.1	599	1	US-08-463-163-3	Sequence 3, Appli
34	728.5	52.4	244	2	US-08-553-497A-20	Sequence 20, Appli
35	726.5	52.2	246	2	US-08-553-497A-24	Sequence 24, Appli
36	720.5	51.8	281	4	US-09-423-439-44	Sequence 44, Appli
37	718	51.6	246	1	US-08-469-486-57	Sequence 57, Appli
38	718	51.6	246	2	US-08-469-486-57	Sequence 57, Appli
39	713.5	51.3	244	2	US-08-553-497A-22	Sequence 22, Appli
40	709.5	51.0	244	2	US-08-553-497A-26	Sequence 26, Appli
41	709.5	51.0	244	4	US-09-244-369B-1	Sequence 1, Appli
42	705	50.7	282	2	US-08-860-174A-10	Sequence 10, Appli
43	698.5	50.2	242	2	US-08-553-497A-28	Sequence 28, Appli
44	696.5	50.1	637	1	US-08-235-838-16	Sequence 16, Appli
45	696.5	50.1	637	2	US-08-465-473B-16	Sequence 16, Appli

ALIGNMENTS

RESULT 1
US-08-257-341-5
; Sequence 5, Application US/08257341
; Patent No. 5525491
; GENERAL INFORMATION:
; APPLICANT: HUSTON, JAMES S
; APPLICANT: OPPERMANN, HERMANN
; APPLICANT: TIMASHEFF, SERGE N
; TITLE OF INVENTION: SERINE RICH PEPTIDE LINKER
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CREATIVE BIOMOLECULES, INC./PATENT DEPT.
; STREET: 35 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,341
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/842,149
; FILING DATE:
; APPLICATION NUMBER: US 07/662,226
; FILING DATE: 27-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL ESQ, PAULA A
; REGISTRATION NUMBER: 32,503
; REFERENCE/DOCKET NUMBER: CRP-064CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000 (ATTY)
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 367 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-257-341-5

Query Match 66.8%; Score 928.5; DB 1; Length 367;

Best Local Similarity 74.7%; Pred. No. 1.1e-79;
Matches 189; Conservative 18; Mismatches 39; Indels 7; Gaps 3;

QY 13 AAASFAAVALQOOSGAELVRPGASVTLSCASGYTFTDYEIHWRQTPVHGLEWIGAID 72

115 A QAPKSDPEVLOQSGPELVKPGASVRMSCKSGYIFDFYMNWVRQSHGKSLDYIGYIS 174
173 PETGCTAYNOKFKDKATVTVDKSSSTAYMELRSLTSDSAVYYY-----TRWFED-WGOG 126
175 PYSVGTYNOKFKGKATLTVDKSSSTAYMELRSLTSDSAVYYCAGSSGNKWMADYWGCHG 234
127 TLVTVAEGKSSGSGSEKPGDVVMTNPLSLPVSLGDAQASISCRSSQSLHSHNGITYLH 186
235 ASVTVSSSG-SSSSGSSSGSDVVMVTQTPLSLPVSLGDAQASISCRSSQSLVHSHNGITYLN 293
187 WYLOKPGOSPKLLIYKVNRFSGVDPDRFSGSGGTDFTLKISRVEAEDLGIVYFCQSSTHV 246
294 WYLOKPGOSPKLLIYKVNRFSGVDPDRFSGSGGTDFTLKISRVEAEDLGIVYFCQSSTHV 353
247 PYTFGGGKLEIK 259
354 PPTFGGKLEIK 366

RESULT 2

US-08-257-341-7
Sequence 7, Application US/08257341
Patent No. 5535491
GENERAL INFORMATION:
APPLICANT: HUSTON, JAMES S
APPLICANT: OPPERMAN, HERMANN
APPLICANT: TIMASHEFF, SERGE N
TITLE OF INVENTION: SERINE RICH PEPTIDE LINKER
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: CREATIVE BIOMOLECULES, INC./PATENT DEPT.
STREET: 35 SOUTH STREET
CITY: HOPKINTON
STATE: MA
COUNTRY: USA
ZIP: 01748
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,341
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/842,149
FILING DATE:
APPLICATION NUMBER: US 07/662,226
FILING DATE: 27-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL ESO, PAULA A
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: CRP-064CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000 (ATTY)
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 246 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-257-341-7

Query Match 66.7%; Score 927.5; DB 1; Length 246;
Best Local Similarity 76.6%; Pred. No. 8e-80;
Matches 187; Conservative 17; Mismatches 33; Indels 7; Gaps 3;
22 VOLQOSGAELVRPGASVTLSCKASGYTFTDYEIHWVRQTPVHGLEWIGAIIDPETGTAYN 81
3 VOLQOSGPELVKPGASVRMSCKSGYIFDFYMNWVRQSHGKSLDYIGYISPYSGVTGN 62

QY 82 QKPKDKATVTVDKSSSTAYMELRSLTSDSAVYYY-----TRWFED-WGOGTLTVSAEG 135
DB 63 QKPKGKATLTVDKSSSTAYMELRSLTSDSAVYYCAGSSGNKWMADYWGCHGASVTVSSSG 122
QY 136 KSSGSGSEKPGDVVMTNPLSLPVSLGDAQASISCRSSQSLHSHNGITYLHMYLQKPGOS 195
DB 123 -SSSSGSSSGSDVVMVTQTPLSLPVSLGDAQASISCRSSQSLVHSHNGITYLNMYLQKAGOS 181
QY 196 PKLLIYKVNRFSGVDPDRFSGSGGTDFTLKISRVEAEDLGIVYFCQSSTHVPTFGGKTK 255
DB 182 PKLLIYKVNRFSGVDPDRFSGSGGTDFTLKISRVEAEDLGIVYFCQSSTHVPTFGGKTK 241
QY 256 LEIK 259
DB 242 LEIK 245

RESULT 3

US-08-133-804-4
Sequence 4, Application US/08133804
Patent No. 5534254
GENERAL INFORMATION:
APPLICANT: Huston, James S.
APPLICANT: Oppermann, Hermann
APPLICANT: Houston, L. L.
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosynthetic Binding Proteins For
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
STREET: Exchange Place, 53 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/133.804
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Kelley, Robin D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: 2054/22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7477
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-133-804-4

Query Match 66.7%; Score 927.5; DB 1; Length 252;
Best Local Similarity 76.6%; Pred. No. 8.3e-80;
Matches 187; Conservative 17; Mismatches 33; Indels 7; Gaps 3;

QY 22 VOLQOSGAELVRPGASVTLSCKASGYTFTDYEIHWVRQTPVHGLEWIGAIIDPETGTAYN 81
DB 3 VOLQOSGPELVKPGASVRMSCKSGYIFDFYMNWVRQSHGKSLDYIGYISPYSGVTGN 62
QY 82 QKPKDKATVTVDKSSSTAYMELRSLTSDSAVYYY-----TRWFED-WGOGTLTVSAEG 135
DB 63 QKPKGKATLTVDKSSSTAYMELRSLTSDSAVYYCAGSSGNKWMADYWGCHGASVTVSSSG 122
QY 136 KSSGSGSEKPGDVVMTNPLSLPVSLGDAQASISCRSSQSLHSHNGITYLHMYLQKPGOS 195

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Db 123 -SSSGSSSGSDVVMVTQTPLSLPVSLGDAQASICRSQSLVHSGNTYLNWYLOKAGQS 181
QY 196 PKLLIYKVSNRFSVGPDRFSGSGGTDTFTLKISRVEADLGVIYFCSTHVPYTFGGGTK 255
Db 182 PKLLIYKVSNRFSVGPDRFSGSGGTDTFTLKISRVEADLGVIYFCSTHVPYTFGGGTK 241
QY 256 LEIK 259
Db 242 LEIK 245

RESULT 4
US-08-461-838-4
; Sequence 4, Application US/08461838
; Patent No. 5753204
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-838-4

Query Match 66.7%; Score 927.5; DB 1; Length 252;
Best Local Similarity 76.6%; Pred. No. 8.3e-80;
Matches 187; Conservative 17; Mismatches 33; Indels 7; Gaps 3;

QY 22 VOLQSGAELVRPGASVTLSCASGYTFTDYEIHVWVQTPVHGLEWICAIIDPETGGTAYN 81
Db 3 VOLQSGPELVKPCASVRMSCKSSGYITDFYMNWVRQSHGKSLDIYIGIYSPYSGVTGYN 62
QY 82 QKFKDKATVTDKSSSTAYMELRSLTSDSAVYYY-----TRWFED-WGQGLTVTVSAEG 135
Db 63 QKFKGKATLTVDKSSSTAYMELRSLTSDSAVYYYCAGSSGNKNWANDYWGHSASVTVSSG 122
QY 136 KSSGSGSESKPGDVMTNPLSLPVSLGDAQASICRSQSLVHSGNTYLNWYLOKAGQS 195
Db 123 -SSSGSSSGSDVVMVTQTPLSLPVSLGDAQASICRSQSLVHSGNTYLNWYLOKAGQS 181
QY 196 PKLLIYKVSNRFSVGPDRFSGSGGTDTFTLKISRVEADLGVIYFCSTHVPYTFGGGTK 255
Db 182 PKLLIYKVSNRFSVGPDRFSGSGGTDTFTLKISRVEADLGVIYFCSTHVPYTFGGGTK 241
QY 256 LEIK 259
Db 242 LEIK 245
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Db 182 PKLLIYKVSNRFSVGPDRFSGSGGTDTFTLKISRVEADLGVIYFCSTHVPYTFGGGTK 241
QY 256 LEIK 259
Db 242 LEIK 245

RESULT 5
US-08-461-386-4
; Sequence 4, Application US/08461386
; Patent No. 5837846
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; TITLE OF INVENTION: Imaging
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 252 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-386-4

Query Match 66.7%; Score 927.5; DB 2; Length 252;
Best Local Similarity 76.6%; Pred. No. 8.3e-80;
Matches 187; Conservative 17; Mismatches 33; Indels 7; Gaps 3;

QY 22 VOLQSGAELVRPGASVTLSCASGYTFTDYEIHVWVQTPVHGLEWICAIIDPETGGTAYN 81
Db 3 VOLQSGPELVKPCASVRMSCKSSGYITDFYMNWVRQSHGKSLDIYIGIYSPYSGVTGYN 62
QY 82 QKFKDKATVTDKSSSTAYMELRSLTSDSAVYYY-----TRWFED-WGQGLTVTVSAEG 135
Db 63 QKFKGKATLTVDKSSSTAYMELRSLTSDSAVYYYCAGSSGNKNWANDYWGHSASVTVSSG 122
QY 136 KSSGSGSESKPGDVMTNPLSLPVSLGDAQASICRSQSLVHSGNTYLNWYLOKAGQS 195
Db 123 -SSSGSSSGSDVVMVTQTPLSLPVSLGDAQASICRSQSLVHSGNTYLNWYLOKAGQS 181
QY 196 PKLLIYKVSNRFSVGPDRFSGSGGTDTFTLKISRVEADLGVIYFCSTHVPYTFGGGTK 255
Db 182 PKLLIYKVSNRFSVGPDRFSGSGGTDTFTLKISRVEADLGVIYFCSTHVPYTFGGGTK 241
QY 256 LEIK 259
Db 242 LEIK 245
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RESULT 6

US-09-070-408-132
; Sequence 132, Application US/09070408
; Patent No. 6180341
; GENERAL INFORMATION:
; APPLICANT: Iverson, Brent L.
; APPLICANT: Georgiou, George
; APPLICANT: Burks, Elizabeth A.
; TITLE OF INVENTION: IN VITRO SCANNING SATURATION MUTAGENESIS
; TITLE OF INVENTION: OF PROTEINS
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070.408
FILING DATE: Concurrently Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/045,409
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: McMillian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: UTSB:593
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/447-7577

INFORMATION FOR SEQ ID NO: 132:
SEQUENCE CHARACTERISTICS:
LENGTH: 269 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear

JS-09-070-408-132

Query Match 61.0%; Score 848.5; DB 4; Length 269;
Best Local Similarity 69.7%; Pred. No. 2.6e-72;
Matches 170; Conservative 23; Mismatches 44; Indels 7; Gaps 3;

2Y 22 VQLQSGAELVRPCASVTLSCKASGYFTDYEHVWROTPVHGLEWIGAITDPETGGTAYN 81

Db 3 VQLQSGPELVKPGASVRMSCKSSGYFTDYVWVWROSHCKSLDYIGYISPSVGTGYN 62

2Y 82 QKFKKAIIVTVKSSSTAYMELRSLTSEDSAVYY-----TRWFD-WGGTILVTVSAG 135

Db 63 QKFKKATLTVKSSSTAYMELRSLTSEDSAVYYCAGSSGNKWMADYVHGCASTVTVSSGG 122

2Y 136 KSSGSGSESKPG-DVWMTNPLSLPVSLGQASISCRSSQSLHNSGITYLHWYLOKPGQ 194

Db 123 GSGSGSGGGGGSDIVLTQTPPLVSLGQATISCRSSQSLVHNSGNTYLVNWLKAGQ 182

2Y 195 SPKLLIYKVSNRFGVPDRFGSGSGDTFTLKISRVAEDLVGYFCSQSTHVPYTFGGGT 254

Db 183 SPKLLIYKVSNRFGVPDRFGSGSGDTFTLKISRVAEDLVGYFCSQSTHVPYTFGGGT 254

2Y 255 KLEI 258

Db 243 KLEI 246

RESULT 7

US-09-423-439-38
; Sequence 38, Application US/09423439
; Patent No. 6339070
; GENERAL INFORMATION:
; APPLICANT: EMERY, Stephen Charles
; BLAREY, David Charles
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pillsbury Winthrop, L.L.P.
; STREET: 1100 New York Ave., N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423.439
FILING DATE: 09-NOV-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997

INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:

US-09-423-439-38

Query Match 59.7%; Score 830; DB 4; Length 288;
Best Local Similarity 64.2%; Pred. No. 1.6e-70;
Matches 174; Conservative 30; Mismatches 55; Indels 12; Gaps 6;

QY 10 LIAAAHSAFAAVQLQSGAELVRPCASVTLSCKASGYFTDYEHVWROTPVHGLEWIG 69

Db 12 LLLAAQAPAAQVQLQPCAEVLKPGASVQLSCASGYFTGTGWIHWVQRPCQGLEWIG 71

QY 70 AIDPETGGTAYNQKFKAIIVTVKSSSTAYMELRSLTSEDSAVYYTR-----WFD--- 122

Db 72 EYNPSTGRSDYNEKFKATLTVKSSSTAYMQLSLSLTSSEDSAVYYCARERAYGYDDAMD 131

QY 123 -WGGTGLTVTVSAGKSSGSGSESKPG-DVWMTNPLSLPVSLGQASISCRSSQSLHNS- 179

Db 132 YWGGTGLTVTVSAGKSSGSGSGGGGGSDIELSQSSSLAVSAGEKVTMCKSSQSLNLR 191

QY 180 NGITYLHWYLOKPGSPKLLIYKVSNRFGVPDRFGSGSGDTFTLKISRVAEDLVGYVF 239

Db 192 TRKNLAWYQORPGQSPKLLIYWASTRTSGVDPDRFGSGSGDTFTLTSSVQAEADLAIVY 251

QY 240 CSQSTHVPYTFGGGTGLEIK-EKLISEEDL 269

Db 252 CKQS-YTLRTFGGTGLEIKREOKLISEEDL 281

RESULT 8

US-08-447-402-1
; Sequence 1, Application US/08447402
; Patent No. 5866344
; GENERAL INFORMATION:
; APPLICANT: Iverson, Brent
; APPLICANT: Georgiou, George
; APPLICANT: Chen, Gang
; TITLE OF INVENTION: IMMUNOASSAY AND ANTIBODY SELECTION

TITLE OF INVENTION: METHODS USING CELL SURFACE EXPRESSED

TITLE OF INVENTION: LIBRARIES

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P. O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/447,402

FILING DATE: 23-MAY-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/258,543

FILING DATE: 10-JUN-1994

CLASSIFICATION: 424

APPLICATION NUMBER: 07/794,731

FILING DATE: 15-NOV-1991

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Kitchell, Barbara S.

REGISTRATION NUMBER: 33,928

REFERENCE/DOCKET NUMBER: UT58\584\KIT

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (512) 474-7577

TELEX: 79-0924

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 260 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-447-402-1

Query Match 58.8%; Score 818.5; DB 2; Length 260;

Best Local Similarity 66.9%; Pred. No. 1.7e-69;

Matches 164; Conservative 26; Mismatches 48; Indels 7; Gaps 3;

QY 22 VQLQSGAELVRPGASVTLSCKASGYTFTDYEIHWRQTPVHGLEWIGAIIDPETGGTAYN 81

DB 2 VQLQSGPELVKPGASVWMSCKSGYIFDYMWRQSHGKSLDYGISPSYSGVTGYN 61

QY 82 QKPKDKAIVTVDKSSSTAYMELRSLTSEDSAVYYY-----TRWFD-WGQGLTVTVSAEG 135

DB 62 QKPKGKATLVTVDKSSSTAYMELRSLTSEDSAVYYCAGSGGNKAWDYWGHCASVTVSSGG 121

QY 136 KSSGSGSESKPG-DVWMTNPLSLPVSLGDOASISCRSSQSLHNSGITYLHWYLOKPGQ 194

DB 122 GSGSGSGSGGGSDIVLTQSPASLAVSLGQRATISCRSSQSLVHNSGNTLYNNYQKPGQ 181

QY 195 SPKLLIYKVSNRFGVDPDRFSGSGSGDTFTLKISRVAEDLGIVYFCQSOTHPVTFGGGT 254

DB 182 PKKLLIYKVSNRFGVDPDRFSGSGSGDTFTLIDPVEDDAIYCSQTHVPTFGSGT 241

QY 255 KLEIK 259

DB 242 KLEIK 246

RESULT 9

US-09-227-693-34

Sequence 34, Application US/09227693

Patent No. 6287562

GENERAL INFORMATION:

APPLICANT: PASTAN, Ira

APPLICANT: BENHAR, Itai

APPLICANT: PADLAN, Eduardo A.

APPLICANT: JUNG, Sun-Hee

APPLICANT: LEE, Byungkook

TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY

TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew

STREET: Stuart Street Tower, One Market Plaza

CITY: San Francisco

STATE: California

COUNTRY: US

ZIP: 94105-1493

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/227,693

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/331,396

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/767,331

FILING DATE: 30-SEP-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/596,289

FILING DATE: 12-OCT-1990

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen Lauver

REGISTRATION NUMBER: 32,762

REFERENCE/DOCKET NUMBER: 15280-126-1-3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 247 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-227-693-34

Query Match 58.0%; Score 806.5; DB 4; Length 247;

Best Local Similarity 63.7%; Pred. No. 2.1e-68;

Matches 156; Conservative 29; Mismatches 53; Indels 7; Gaps 2;

QY 22 VQLQSGAELVRPGASVTLSCKASGYTFTDYEIHWRQTPVHGLEWIGAIIDPETGGTAYN 81

DB 3 VKLVESSGGLVQPGSLKLSKATSGFTFSDYMYWVRQTPKRLWVAYISNDSSAAYS 62

QY 82 QKPKDKAIVTVDKSSSTAYMELRSLTSEDSAVYYYR-----WFDWGQGLTVTVSAEG 135

DB 63 DTYKGRFTISRDNARNTLYLQMSRLKSEDTAIYSCARGLAWGAWFAYWGQGLTVTVSSGG 122

QY 136 KSSGSGSESKPG-DVWMTNPLSLPVSLGDOASISCRSSQSLHNSGITYLHWYLOKPGQ 194

DB 123 GSGSGSGSGGGSDIVLTQSPASLAVSLGQASISCRSQIIVHNSGNTLYLWYLOKPGQ 182

QY 195 SPKLLIYKVSNRFGVDPDRFSGSGSGDTFTLKISRVAEDLGIVYFCQSOTHPVTFGGGT 254

DB 183 SPKLLIYKVSNRFGVDPDRFSGSGSGDTFTLKISRVAEDLGIVYFCQSHVPTFGSGT 242

QY 255 KLEIK 259

DB 243 KLEIK 247

RESULT 10

US-08-331-398A-34

RESULT 12
US-08-759-804A-34
; Sequence 34, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-759-804A-34
Query Match 58.0%; Score 806.5; DB 2; Length 248;
Best Local Similarity 63.7%; Pred. No. 2.1e-66;
Matches 156; Conservative 29; Mismatches 53; Indels 7; Gaps 2;
QY 22 VLOQSGAELVRPGASVTLSCKASGYTFDYEIHWVROTYPVHGLEWIGATDPETGTAYN 81
DB 3 KLVESGGGLVQPGSKLSKATSGFTFSDYMYWVROTPEKRLWEVAYISNDSSAAYS 62
QY 82 QKFKDKAIVTVDKSSSTAYMELRLSTSEDSAVYYTR-----WFDWGQGTTLTVSAEG 135
DB 63 DTVKGRFTISRDNARNTLYLQMSRLKSEDTAIYSCARGLANWAFYWGQGTTLTVSSGG 122
QY 136 KSSGSGSEKPG-DVWMTNPPLSLPVSLGDAQSISCRSSQSLHNSGITYLHWYLRPGQ 194
DB 123 GSGGGGGGGGGSDVLMQTQSPSLSPVSLGDAQSISCRSSQIIVHNSGNTYLEWYLRPGQ 182
QY 195 SPKLLIYKVSNNRFGVDPDRFSGSGSGDTFTLKISRVEAEDLGVVFCQSOSTHVPYTFGGGT 254
DB 183 SPKLLIYKVSNNRFGVDPDRFSGSGSGDTFTLKISRVEAEDLGVVYFCQGHVPTFGSGT 242

QY 255 KLEIK 259
DB 243 KLEIK 247
RESULT 13
US-09-070-637-20
; Sequence 20, Application US/09070637A
; Patent No. 6132722
; GENERAL INFORMATION:
; APPLICANT: SIEMERS, NATHAN O.
; APPLICANT: YARNOLD, SUSAN
; APPLICANT: SENTER, PETER D.
; TITLE OF INVENTION: RECOMBINANT ANTIBODY-ENZYME FUSION PROTEINS
; FILE REFERENCE: 9197F-83-1
; CURRENT APPLICATION NUMBER: US/09/070,637A
; CURRENT FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: 60/045,888
; EARLIER FILING DATE: 1997-05-07
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence for L49-sfv-bl including Pe1B leader
US-09-070-637-20
Query Match 56.7%; Score 788.5; DB 4; Length 638;
Best Local Similarity 60.4%; Pred. No. 3.9e-66;
Matches 165; Conservative 31; Mismatches 60; Indels 17; Gaps 5;
QY 10 LLAASAFAPAAVLOQSGAELVRPGASVTLSCKASGYTFDYEIHWVROTYPVHGLEWIG 69
DB 12 LLLAQAQPAWAEVQLOESGPSLVKPSQTLSTCSVTGDSITSGYWNWIRKFGPKLEYMG 71
QY 70 AIDPETGTAYNQKFKDKAIVTVDKSSSTAYMELRLSTSEDSAVY-----YYTRWF 120
DB 72 YIS-DSGITYNPSLSKSRISITRDTSKNQYVQLNFVTAEDTATYNCARRTLATYYA--M 128
QY 121 EDWGQGTTLTVSAEGKSS-----CSGSEKPGDVWMTNPPLSLPVSLGDAQSISCRSSQSL 176
DB 129 DYWGQGTSTVTSSGSGTSGSGKPGSGEGSTKGDFVMTQTPLSLPVSLGDAQSISCRASQSL 188
QY 177 LHSNGITYLHWYLRPGQSPKLLIYKVSNNRFGVDPDRFSGSGSGDTFTLKISRVEAEDLG 236
DB 189 VHSNGNTYLHWYLRPGQSPKLLIYKVSNNRFGVDPDRFSGSGSGDTFTLKISRVEAEDLG 248
QY 237 VYFCQSOSTHVPYTFGGGTLEIKKEKLISEEDL 269
DB 249 VYFCQSOSTHVPYTFGGGTLEIKRTP-VSEKQL 280
RESULT 14
US-08-983-035A-38
; Sequence 38, Application US/08983035A
; Patent No. 6326464
; GENERAL INFORMATION:
; APPLICANT: CONSEILLER, EMMANUEL
; BRACCO, LAURENT
; TITLE OF INVENTION: P53 PROTEIN VARIANTS AND THERAPEUTICAL
; USES THEREOF
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT &
; DUNNER, LLP
; STREET: 1300 I Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/983,035A
FILING DATE: 20-Feb-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR96/01111
FILING DATE: 17-JUL-1996
APPLICATION NUMBER: FR 95/08729
FILING DATE: 19-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Strauss, William L.
REGISTRATION NUMBER: 47,114
REFERENCE/DOCKET NUMBER: 03804.0142
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 535 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
US-08-983-035A-38

Query Match 56.6%; Score 788; DB 4; Length 535;
Best Local Similarity 65.2%; Pred. No. 3.4e-66;
Matches 159; Conservative 24; Mismatches 57; Indels 4; Gaps 2;

QY 20 AAQLQSGAELVPCASVTLSCASGYFTDYIEIHWVROTPVHGLEWICADPETGGTA 79
DB 2 AQVLQSGAELVPCASVTLSCASGYFTDYIEIHWVROTPVHGLEWICADPETGGTA 61

QY 80 YNOKFKDKAIVTVDKSSSTAYMELRLTSEDSAVYY---YTRWFEDWGQOTLVTSAGK 136
DB 62 YAPKFGKATMTADTSNTAYLQLSLASEDTAVYYCNFYGDALDWGQOTLVTSAGG 121

QY 137 SSGSGSEKPG-DVWTPNPLSLPVLGDOASISCRSSQSLHSHNGITYLHWYLPKPGOS 195
DB 122 GSGGGSGGGGSDVLTQTPLTSLVTIGOPASISCKSSQSLDSDGKTYLNMLLQRPQOS 181

QY 196 PKLLIYKVNRFSGVDRFSGSGGDTFTLKISRVEADLGVYFCQSSTHVPYTFGGTK 255
DB 182 PKRLIYLVSKLSDGVDRFSGSGGDTFTLKISRVEADLGVYFCQSSTHVPYTFGGTK 241

QY 256 LEIK 259
DB 242 LEUK 245

RESULT 15
US-09-423-439-32
Sequence 32, Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-No. 6339070-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 673 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-423-439-32

Query Match 56.0%; Score 779.5; DB 4; Length 673;
Best Local Similarity 61.1%; Pred. No. 2.9e-65;
Matches 160; Conservative 32; Mismatches 59; Indels 11; Gaps 5;

QY 8 YVLLAAAHSAFAAVALQOOSGAELVPCASVTLSCASGYFTDYIEIHWVROTPVHGLEW 67
DB 7 WIFLVTLINGIQCVQLQOPGAELVPCASVTLSCASGYFTGTGWIHWKORPQGGLEW 66

QY 68 IGAIIDPETGGTAYNOKFKDKAIVTVDKSSSTAYMELRLTSEDSAVYYTR---WFED- 122
DB 67 ICEVNPSTGRSDYNEKFKNKATLTVDKSTTAYMQLSSLTSEDSAVYYCARERAYGDDA 126

QY 123 ---WGQOTLVTVSAEKGSGSGSEKPG-DVWTPNPLSLPVLGDOASISCRSSQSLH 178
DB 127 MDYWGQOTLVTVSSGGGSGGGGSDIELSPSSLAVSAGEKVTMSCKSSQSLN 186

QY 179 S-NGITYLHWYLPKPGOSPKLLIYKVNRFSGVDRFSGSGGDTFTLKISRVEADLGV 237
DB 187 SRTKKNYLANWQORFGOSPKLLIYWASTRTSGVDRFSGSGGDTFTLTSSVQAEADLAI 246

QY 238 YFCQSSTHVPYTFGGTKLEIK 259
DB 247 YYCKQS-YTLRTFGGTKLEIK 267

Search completed: May 16, 2003, 14:26:53
Job time : 32 secs